



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 106612

To: Sumesh Kaushal
Location: CM1/12A07/11E12
Art Unit: 1636
Tuesday, October 28, 2003

Case Serial Number: 09/925674

From: Beverly Shears
Location: Biotech-Chem Library
CM1-1E05
Phone: 308-4994

beverly.shears@uspto.gov

Search Notes

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 24, 2003, 10:27:45 : Search time 60 seconds
(without alignments)
510.570 Million cell updates/sec

Title: US-09-925-674A-7
Perfect score: 1007
Sequence: 1 MATPASAPCTRALVADFGV.....LTGAVALCALVTVGAEFFASK 193

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_13Jun03.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	1007	100.0	193	AA05530	Human Bcl-w protei
2	1002	99.5	193	AAW61392	Human bcl-y protei
3	1002	99.5	193	AAW97392	The human bcl-y pr
4	1000	99.3	193	AAW36047	Human bcl-w protei
5	1000	99.3	193	AA05531	Mouse Bcl-w protei
6	1000	99.3	193	AA05532	Human Bcl-w protei
7	997	99.0	192	AAW97394	Mammalian bcl-y pr
8	996	98.9	193	AAW61391	Rat bcl-y protein.
9	996	98.9	193	AAW97391	The rat bcl-y prot

10	991	98.4	192	20	AAW97393	Protein sequence o
11	958.5	95.2	192	20	AA05533	Mouse Bcl-w protei
12	867	86.1	168	18	AAW36048	Mouse bcl-w protei
13	821.5	81.6	190	23	AAO18223	Human Bcl-Rambo BH
14	766	76.1	365	19	AAW59884	Amino acid sequenc
15	766	76.1	365	23	ABG95556	Human novel secret
16	433.5	43.0	411	22	AAU00219	Bcl-X1-DTR apoptos
17	431.5	42.9	237	23	ABG78480	wild type BclX1 pr
18	428.5	42.6	233	16	ABG68887	Human thymus BCL-X
19	428.5	42.6	233	17	AAW05821	Bcl-XL protein. H
20	428.5	42.6	233	18	AAW31530	Human anti-apoptot
21	428.5	42.6	233	21	AAW81223	Bcl-x polypeptide.
22	428.5	42.6	233	21	AAW69969	Human Bcl-XL prote
23	428.5	42.6	233	22	AAW64262	Human Bcl-XL prote
24	428.5	42.6	233	22	AAW73303	Rat wild-type Bcl-
25	428.5	42.6	233	22	AAW50538	Human Bcl-XL prote
26	428.5	42.6	233	22	AAW47515	Protein encoded by
27	425	42.2	225	18	AAW19396	"Deprenyl" (RIM)-1
28	424.5	42.2	233	22	AAW73304	Mutant rat Bcl-XL
29	416.5	41.4	239	22	AAW64037	Human Bcl-2 protei
30	415.5	41.3	152	24	AAW79760	Bcl-XL. Homo sapi
31	413	41.0	236	22	AAW35131	Murine Bcl-2. Mus
32	413	41.0	236	23	AAW76554	Murine Bcl-2 polyp
33	412.5	41.0	239	20	AAW87810	A human Bcl-2 prot
34	412.5	41.0	239	22	AAW74127	Human Bcl-2. Homo
35	412.5	41.0	239	22	AAW35130	Human Bcl-2. Homo
36	412.5	41.0	239	23	ABG78478	Human Bcl2 mutant
37	412.5	41.0	239	23	ABG78479	Human Bcl2 mutant
38	412.5	41.0	239	23	AAW76553	Human Bcl-2 polyt
39	412.5	41.0	272	24	ABW41675	Human DITHP cell m
40	410.5	40.8	239	9	AAW80387	Sequence of Bcl-2-
41	410.5	40.8	239	14	AAW42312	Bcl-2 oncogene pro
42	410.5	40.8	239	16	AAW70331	Human bcl-2 protei
43	410.5	40.8	239	16	AAW71404	Human bcl-2 alpha
44	410.5	40.8	239	19	AAW40217	Human bcl-2. Homo
45	410.5	40.8	239	20	AAW87812	A human Bcl-2-alph

ALIGNMENTS

RESULT 1
AA05530
ID AA05530 standard; Protein; 193 AA.
XX
AC AA05530;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human Bcl-w protein essential for spermatogenesis.
XX
KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW animal model.
XX
OS Homo sapiens.
XX
PN W09913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU00764.
XX
PR 16-SEP-1997; 97AU-0009228.
XX
FA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
XX
DR WP; 1999-243890/20.
DR N-PSDB; AAW25132.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
protein associated with Bcl-w

XX Claim 2; Page 33; 52pp; English.

XX The present sequence is human Bcl-w, a pro-survival member of the
XX Bcl-2 family which is widely expressed and which is essential for
XX spermatogenesis. The invention relates generally to a method of
XX treatment and to an animal model for the identification of
XX molecules and genetic sequences useful for inducing or reducing
XX fertility of male animals. Methods are provided for the treatment
XX of infertility, or for reducing fertility, by modulating
XX spermatogenesis. An animal model carries a mutation is at least
XX one allele of the human or murine bcl-w gene (see AAX5132-35) or in
XX a gene associated with bcl-w. Such animals have disorganised
XX seminiferous tubules and are substantially infertile, but possess no
XX other major abnormalities as determined by histological examination.
XX They can be used to screen for therapeutic molecules including
XX genetic sequences capable of inducing, enhancing or otherwise
XX facilitating spermatogenesis in animals, or which can induce
XX infertility.

XX Sequence 193 AA;

Query Match 100.0%; Score 1007; DB 20; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.4e-103;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60
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DB 61 FSDLAQLHVTGSAOQRTQVSDDELFOGPNWGRVLAFFVFGAALCAESVNKEMEPLVG 120
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DB 121 QVQEMWVAYLETRLADWIHSSGWAFFETALYDGGALEEARRLRGNWASVRTVLTGAVAL 180
QY 181 GALVTVGAFASK 193
DB 181 GALVTVGAFASK 193

RESULT 2

AAW61392
ID AAW61392 standard; Protein; 193 AA.

XX AAW61392;

XX 02-OCT-1998 (first entry);

XX Human bcl-y protein.

XX bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.

XX Homo sapiens.

XX US5789201-A.

XX 04-AUG-1998.

XX 11-FEB-1997; 97US-0798897.

XX 23-FEB-1996; 96US-0012201.

XX 11-FEB-1997; 97US-0798897.

XX (COCE-) COCENSYS INC.

XX Guastella J;

XX WPI; 1998-446079/38.

XX N-PSDB; AAV28334.

XX

PT Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT producing recombinant protein for use in treating uncontrolled cell
PT growth e.g. cancers

XX Example; Column 17/18; 27pp; English.

XX The mammalian bcl-y protein is a member of the bcl-2 family, components
XX in the cell death pathway. The bcl-2 family have both apoptotic activity
XX and the apoptosis blocking activity. bcl-y falls in the apoptosis
XX activity category. The recombinant protein may be used to prevent
XX uncontrolled cell growth, either by its direct administration to
XX recombinant genetic constructs to increase its expression in vivo. Also,
XX antisense constructs can be used in disorders where prevention of cell
XX death is desired.

XX Sequence 193 AA;

Query Match 99.5%; Score 1002; DB 19; Length 193;
Best Local Similarity 99.5%; Pred. No. 1.2e-102;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHVTGSAOQRTQVSDDELFOGPNWGRVLAFFVFGAALCAESVNKEMEPLVG 120
DB 61 FSDLAQLHVTGSAOQRTQVSDDELFOGPNWGRVLAFFVFGAALCAESVNKEMEPLVG 120
QY 121 QVQEMWVAYLETRLADWIHSSGWAFFETALYDGGALEEARRLRGNWASVRTVLTGAVAL 180
DB 121 QVQEMWVAYLETRLADWIHSSGWAFFETALYDGGALEEARRLRGNWASVRTVLTGAVAL 180
QY 181 GALVTVGAFASK 193
DB 181 GALVTVGAFASK 193

RESULT 3

AAW97392
ID AAW97392 standard; Protein; 193 AA.

XX AAW97392;

XX 20-MAY-1999 (first entry);

XX The human bcl-y protein.

XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
XX head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
XX multiple sclerosis; myocardial infarction; vitally induced cell death;
XX aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
XX premature cell death; cell death stimulator; prolonged cell life span;
XX Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
XX parasite.

XX Homo sapiens.

XX US588329-A.

XX 16-MAR-1999.

XX 25-NOV-1997; 97US-0978523.

XX 23-FEB-1996; 96US-0012201.

XX 11-FEB-1997; 97US-0798897.

XX 25-NOV-1997; 97US-0978523.

XX (COCE-) COCENSYS INC.

XX Guastella J;

XX

DR WPI; 1999-214150/18.
 XX N-PSDB; AAX15946.
 PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
 PT for modulating programmed cell death
 XX
 PS Claim 1; Columns 17-18; 26pp; English.
 XX
 CC The present sequence represents human bcl-y protein (Hbcl-y). The
 CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and
 CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
 CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
 CC proteins may be used to treat conditions associated with a disruption of
 CC the cell death pathway. If they act as cell death inhibitors, they may be
 CC used in therapies to treat subjects suffering from: strokes, head trauma,
 CC Alzheimer's disease, neural and muscular degenerative diseases
 CC (especially multiple sclerosis), myocardial infarction, vitally induced
 CC cell death, aging, spinal cord injuries and amyotrophic lateral
 CC sclerosis- conditions where cells under go premature cell death as a
 CC result of triggers which may or may not be apparent. They may also be
 CC used in this way to develop cell lines which remain viable in culture for
 CC an extended period. In contrast, if they act as cell death stimulators,
 CC Rbcl-y and Hbcl-y may be used to treat conditions associated with
 CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and
 CC lung cancer) and auto/hyperimmune diseases. They may also be used to
 CC cause cell death in, and hence control, parasites.
 XX
 SQ Sequence 193 AA;
 Query Match 99.5%; Score 1002; DB 20; Length 193;
 Best Local Similarity 99.5%; Pred. No. 1.2e-102;
 Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60
 Db 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60
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 Db 61 FSDLAALQLHVTGSAQORFTQVSDLELFOGGPNWGRVAFVFGAALCAESVNKEMEPLVG 120
 2y 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGAVAL 180
 Db 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGAVAL 180
 2y 181 GALVTVGAFPAASK 193
 Db 181 GALVTVGAFPAASK 193
 RESULT 4
 AAW36047
 D AAW36047 standard; Protein; 193 AA.
 X
 AC AAW36047;
 X
 T 22-APR-1998 (first entry)
 X
 E Human bcl-w protein.
 X
 W Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
 W diagnosis; degenerative disease.
 W
 S Homo sapiens.
 X
 N WO9735971-A1.
 X
 D 02-OCT-1997.
 X
 F 27-MAR-1997; 97WO-AU00199.
 X
 R 27-MAR-1996; 96AU-0008965.
 X

PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX
 PI Adams JM, Cory S, Gibson LM, Holmgreen SP;
 XX
 DR WPI; 1997-489635/45.
 DR N-PSDB; AAT96577.
 XX
 PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce
 PT or inhibit cell survival, e.g. for treatment of cancer and
 PT degenerative diseases
 XX
 PS Claim 6; Page 48; 86pp; English.
 XX
 CC This sequence represents a novel human protein, bcl-w, encoded by the
 CC bcl-2 gene family and extracted from an adult brain library. This gene
 CC promotes cell survival, so its modulation is useful in treatment of
 CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,
 CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
 CC ischaemia, human immunodeficiency virus infection or in cell transplants.
 CC Up-regulation of the gene can also be used to modify cell lines cultured
 CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
 CC and to increase survival of primary explants during genetic modification.
 CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
 CC antibody production or screening of potential modulators.
 XX
 SQ Sequence 193 AA;
 Query Match 99.3%; Score 1000; DB 18; Length 193;
 Best Local Similarity 99.0%; Pred. No. 2e-102;
 Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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 Db 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60
 Qy 61 FSDLAALQLHVTGSAQORFTQVSDLELFOGGPNWGRVAFVFGAALCAESVNKEMEPLVG 120
 Db 61 FSDLAALQLHVTGSAQORFTQVSDLELFOGGPNWGRVAFVFGAALCAESVNKEMEPLVG 120
 Qy 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGAVAL 180
 Db 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGAVAL 180
 Qy 181 GALVTVGAFPAASK 193
 Db 181 GALVTVGAFPAASK 193
 RESULT 5
 AAY05531
 ID AAY05531 standard; Protein; 193 AA.
 XX
 AC AAY05531;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Mouse Bcl-w protein essential for spermatogenesis.
 XX
 KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
 KW animal model.
 XX
 OS Mus sp.
 XX
 PN WO9913710-A1.
 XX
 PD 25-MAR-1999.
 XX
 PF 16-SEP-1998; 98WO-AU00764.
 XX
 PR 16-SEP-1997; 97AU-0009228.
 XX
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX

PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
 XX WPI; 1999-243890/20.
 DR N-PSDB; AAX25133.
 XX
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 XX protein associated with Bcl-w
 XX
 PS Claim 2; Page 35; 52pp; English.
 XX
 CC The present sequence is mouse Bcl-w, a pro-survival member of the
 CC Bcl-2 family which is widely expressed and which is essential for
 CC spermatogenesis. The invention relates generally to a method of
 CC treatment and to an animal model for the identification of
 CC molecules and genetic sequences useful for inducing or reducing
 CC fertility of male animals. Methods are provided for the treatment
 CC of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation in at least
 CC one allele of the human or murine bcl-w gene (see AAX25132-35) or in
 CC a gene associated with bcl-w. Such animals have disorganised
 CC seminiferous tubules and are substantially infertile, but possess no
 CC other major abnormalities as determined by histological examination.
 CC They can be used to screen for therapeutic molecules including
 CC genetic sequences capable of inducing, enhancing or otherwise
 CC facilitating spermatogenesis in animals, or which can induce
 CC infertility.
 XX
 XX Sequence 193 AA;

Query Match 99.3%; Score 1000; DB 20; Length 193;
 Best Local Similarity 99.0%; Pred. No. 2e-102;
 Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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 DB 1 MATPASPTDTRALVADVGVYKLRQKGVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
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 QY 121 QVQEMVAYLETRLDWIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTCGAVL 180
 DB 121 QVQEMVAYLETRLDWIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTCGAVL 180
 QY 181 GALVTVGAFPAASK 193
 DB 181 GALVTVGAFPAASK 193

RESULT 6
 AAY05532
 ID AAY05532 standard; Protein; 193 AA.

XX
 XX AAY05532;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human Bcl-w protein essential for spermatogenesis.
 XX
 KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
 KW animal model.
 XX
 XX Homo sapiens.
 XX OS
 XX MO9913710-A1.
 XX
 XX 25-MAR-1999.
 XX PD
 XX 16-SEP-1998; 98WO-AU00764.
 XX PF
 XX 16-SEP-1997; 97AU-0009228.
 XX PR
 XX

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX Adams J, Cory S, Gibson L, Koentgen F, Print C;
 XX WPI; 1999-243890/20.
 DR N-PSDB; AAX25134.
 XX
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 XX protein associated with Bcl-w
 XX
 PS Disclosure; Page 37; 52pp; English.
 XX
 CC The present sequence is described of a derivative of human Bcl-w
 CC (see also AAY05530), a pro-survival member of the Bcl-2 family that
 CC is widely expressed and which is essential for spermatogenesis.
 CC The invention relates generally to a method of treatment and to an
 CC animal model for the identification of molecules and genetic
 CC sequences useful for inducing or reducing fertility of male animals.
 CC Methods are provided for the treatment of infertility, or for
 CC reducing fertility, by modulating spermatogenesis. An animal model
 CC carries a mutation in at least one allele of the human or murine
 CC bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w.
 CC Such animals have disorganised seminiferous tubules and are
 CC substantially infertile, but possess no other major abnormalities
 CC as determined by histological examination. They can be used to
 CC screen for therapeutic molecules including genetic sequences
 CC capable of inducing, enhancing or otherwise facilitating
 CC spermatogenesis in animals, or which can induce infertility.
 XX
 XX Sequence 193 AA;

Query Match 99.3%; Score 1000; DB 20; Length 193;
 Best Local Similarity 99.0%; Pred. No. 2e-102;
 Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MATPASAPDTRALVADVGVYKLRQKGVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
 DB 1 MATPASAPDTRALVADVGVYKLRQKGVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
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 DB 181 GALVTVGAFPAASK 193

RESULT 7
 AAW97394
 ID AAW97394 standard; Protein; 192 AA.

XX
 XX AAW97394;
 XX
 AC AAW97394;
 XX
 DT 20-MAY-1999 (first entry)
 XX
 DE Mammalian bcl-y protein.
 XX
 KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
 KW parasite.
 XX
 OS Mammalia.
 XX

```

PN US5883229-A.
XX
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PD 16-MAR-1999.
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XX
PF 25-NOV-1997; 97US-0978523.
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PR 23-FEB-1996; 96US-0012201.
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PR 11-FEB-1997; 97US-0798897.
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PR 25-NOV-1997; 97US-0978523.
XX
XX
PA (COCE-) COCENSYS INC.
XX
XX
PI Guastella J;
XX
XX
DR WPI; 1999-214150/18.
XX
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
PT for modulating programmed cell death
XX
XX
PS Claim 2; Columns 19-22; 26pp; English.
XX
XX
CC The present sequence represents a mammalian bcl-1 protein.
CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein.
CC thought to be involved in programmed cell death (apoptosis and necrosis).
CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
CC with a disruption of the cell death pathway. If they act as cell death
CC inhibitors, they may be used in therapies to treat subjects suffering
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC degenerative diseases (especially multiple sclerosis), myocardial
CC infarction, vitally induced cell death, aging, spinal cord injuries and
CC amyotrophic lateral sclerosis- conditions where cells under go premature
CC cell death as a result of triggers which may or may not be apparent.
CC They may also be used in this way to develop cell lines which remain
CC viable in culture for an extended period. In contrast, if they act as
CC cell death stimulators, Rbcl-y and Hbcl-y may be used to treat
CC conditions associated with prolonged cell life span such as cancer
CC (especially Kaposi's sarcoma and lung cancer) and auto/hyperimmune
CC diseases. They may also be used to cause cell death in, and hence
CC control, parasites.
XX
XX
SQ Sequence : 92 AA;
Query Match 99.0%; Score 997; DB 20; Length 192;
Seq: Local Similarity 99.5%; Pred. No. 4.3e-102;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAAMRAAGDEFETRFRRTF 61
DB 1 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAAMRAAGDEFETRFRRTF 60
QY 62 SDLAAQLHVTTPGSAQQRFTQVSDELFGQGNWGRJVAFFVFGAALCAESVNKEMEPLVG 121
DB 61 SDLAAQLHVTTPGSAQQRFTQVSDELFGQGNWGRJVAFFVFGAALCAESVNKEMEPLVG 120
QY 122 VQEWKVAYLETRLDWIHSSGGWAEFTALYGDGALEAEARLRGNWASVRTVLTGVALG 181
DB 121 VQEWKVAYLETRLDWIHSSGGWAEFTALYGDGALEAEARLRGNWASVRTVLTGVALG 180
QY 182 ALVTGGAFFASK 193
DB 181 ALVTGGAFFASK 192
RESULT 8
AAW61391
ID AAW61391 standard; Protein; 193 AA.
XX
XX
AC AAW61391;
XX
XX
DT 02-OCT-1998 (first entry)
XX
XX
DE Rat bcl-y protein.

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XX bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
XX Rattus sp.
XX
XX US5789201-A.
XX
XX 04-AUG-1998.
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XX 11-FEB-1997; 97US-0798897.
XX
XX 23-FEB-1996; 96US-0012201.
XX
XX 11-FEB-1997; 97US-0798897.
XX
XX (COCE-) COCENSYS INC.
XX
XX Guastella J;
XX
XX WPI; 1998-446079/38.
XX
XX N-PSDB; AAV28333.
XX
XX Nucleic acids encoding B-cell lymphoma-y protein - useful for
XX producing recombinant protein for use in treating uncontrolled cell
XX growth e.g. Cancers
XX
XX Example; Fig 3A; 27pp; English.
XX
XX The mammalian bcl-y protein is a member of the bcl-2 family, components
XX in the cell death pathway. The bcl-2 family have both apoptotic activity
XX and the apoptosis blocking activity. bcl-y falls in the apoptosis
XX activity category. The recombinant protein may be used to prevent
XX uncontrolled cell growth, either by its direct administration to
XX recombinant genetic constructs to increase its expression in vivo. Also,
XX antisense constructs can be used in disorders where prevention of cell
XX death is desired.
XX
XX SQ Sequence : 93 AA;
Query Match 98.9%; Score 996; DB 19; Length 193;
Seq: Local Similarity 98.4%; Pred. No. 5.6e-102;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAAMRAAGDEFETRFRRT 60
DB 1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAAMRAAGDEFETRFRRT 60
QY 61 FSDLAAQLHVTTPGSAQQRFTQVSDELFGQGNWGRJVAFFVFGAALCAESVNKEMEPLVG 120
DB 61 FSDLAAQLHVTTPGSAQQRFTQVSDELFGQGNWGRJVAFFVFGAALCAESVNKEMEPLVG 120
QY 122 VQEWKVAYLETRLDWIHSSGGWAEFTALYGDGALEAEARLRGNWASVRTVLTGVAL 180
DB 121 VQODMMVYILETRLDWIHSSGGWAEFTALYGDGALEAEARLRGNWASVRTVLTGVAL 190
QY 181 GALVTGGAFFASK 193
DB 181 GALVTGGAFFASK 193
RESULT 9
AAW97391
ID AAW97391 standard; Protein; 193 AA.
XX
XX AAW97391;
XX
XX 20-MAY-1999 (first entry)
XX
XX The rat bcl-y protein.
XX
XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
XX head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
XX multiple sclerosis; myocardial infarction; vitally induced cell death;

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KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
 KW parasite.

OS Rattus sp.

PN US5883229-A.

PD 16-MAR-1999.

XX 25-NOV-1997; 97US-0378523.

XX 23-FEB-1996; 96US-0012201.

PR 11-FEB-1997; 97US-0798897.

PR 25-NOV-1997; 97US-0378523.

XX (COCE-) COCENSYS INC.

XX Guastella J;

XX WPI; 1999-214150/18.

DR N-PSDB; AAX15945.

XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful

PT for modulating programmed cell death

XX Disclosure; Columns 15-18; 26pp; English.

CC The present sequence represents rat bcl-y protein (Rbcl-y). The
 CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
 CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
 CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
 CC proteins may be used to treat conditions associated with a disruption of
 CC the cell death pathway. If they act as cell death inhibitors, they may be
 CC used in therapies to treat subjects suffering from: strokes, head trauma,
 CC Alzheimer's Disease, neural and muscular degenerative diseases
 CC (especially multiple sclerosis), myocardial infarction, vitally induced
 CC cell death, aging, spinal cord injuries and amyotrophic lateral
 CC sclerosis- conditions where cells under go premature cell death as a
 CC result of triggers which may or may not be apparent. They may also be
 CC used in this way to develop cell lines which remain viable in culture for
 CC an extended period. In contrast, if they act as cell death stimulators,
 CC Rbcl-y and Hbcl-y may be used to treat conditions associated with
 CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and
 CC lung cancer) and auto/hyperimmune diseases. They may also be used to
 CC cause cell death in, and hence control, parasites.

XX Sequence 193 AA;

Query Match 98.98; Score 996; DB 20; Length 193;

Best Local Similarity 98.4%; Pred. No. 5.6e-102; Mismatches 0; Gaps 0;

Matches 190; Conservative 1; Mismatches 2; Indels 0;

1 MATPASAPDTRALVADVFGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

1 MATPASPTDTRALVADVFGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

61 FSDLAQLHVTTPGSAQQRFTQVSDLELFOGGPNWGRVLAFFVFGAALCAESVNKEMEPLVG 120

61 FSDLAQLHVTTPGSAQQRFTQVSDLELFOGGPNWGRVLAFFVFGAALCAESVNKEMEPLVG 120

121 QVQEMVAYLETRLADMIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGVAL 180

121 QVQDMVTYLETRLADMIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGVAL 180

181 GALVTVGAFPAASK 193

181 GALVTVGAFPAASK 193

RESULT 10

AAW97393

ID AAW97393 standard; Protein; 192 AA.

XX AC AAW97393;

XX 20-MAY-1999 (first entry)

XX Protein sequence of the specification.

XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;

XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;

XX head trauma; Alzheimer's Disease; neural; muscular degenerative disease;

XX multiple sclerosis; myocardial infarction; vitally induced cell death;

XX aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;

XX premature cell death; cell death stimulator; prolonged cell life span;

XX Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;

XX parasite.

XX Unidentified.

XX US5883229-A.

XX 16-MAR-1999.

XX 25-NOV-1997; 97US-0378523.

XX 23-FEB-1996; 96US-0012201.

XX 11-FEB-1997; 97US-0798897.

XX 25-NOV-1997; 97US-0378523.

XX (COCE-) COCENSYS INC.

XX Guastella J;

XX WPI; 1999-214150/18.

XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful

XX for modulating programmed cell death

XX Disclosure; Columns 19-20; 26pp; English.

CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
 CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
 CC thought to be involved in programmed cell death (apoptosis and necrosis).
 CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
 CC with a disruption of the cell death pathway. If they act as cell death
 CC inhibitors, they may be used in therapies to treat subjects suffering
 CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
 CC degenerative diseases (especially multiple sclerosis), myocardial
 CC infarction, vitally induced cell death, aging, spinal cord injuries and
 CC amyotrophic lateral sclerosis- conditions where cells under go premature
 CC cell death as a result of triggers which may or may not be apparent.
 CC They may also be used in this way to develop cell lines which remain
 CC viable in culture for an extended period. In contrast, if they act as
 CC cell death stimulators, Rbcl-y and Hbcl-y may be used to treat
 CC conditions associated with prolonged cell life span such as cancer
 CC (especially Kaposi's sarcoma and lung cancer) and auto/hyperimmune
 CC diseases. They may also be used to cause cell death in, and hence
 CC control, parasites.

XX Sequence 192 AA;

Query Match 98.4%; Score 991; DB 20; Length 192;

Best Local Similarity 98.4%; Pred. No. 2e-101;

Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

2 ATPASAPDTRALVADVFGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 61

1 ATPASTDTRALVADVFGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

62 SDLAQLHVTTPGSAQQRFTQVSDLELFOGGPNWGRVLAFFVFGAALCAESVNKEMEPLVG 121

61 SDLAQLHVTTPGSAQQRFTQVSDLELFOGGPNWGRVLAFFVFGAALCAESVNKEMEPLVG 120

1 MPTPASTPDTRALVADFVGVRLRQGVYVCGAGPEGPAADPLHQAVRAACDEFETFRPT 60

2b

2c

2d

61 FSDLAALQHVTPGSAQOORTQVSDLEFQGGPNWGRLVAFVFGAALCAESYNKEMEPLVG 120

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61 FSDLAQLHVTPGSAQQRFTQVSDelfQGGPNWRLVAFVFGAALCAESVKNEMEPLV

QY 121 QVQEWVAYLETRADWIHSSGGWAEFTALYGDGALEEARLRREGNWA 168
DB 121 QVQEWVAYLETRADWIHSSGGWAEFTALYGDGALEEARLRREGNWA 168

RESULT 13
AAO18223
ID AAO18223 standard; Protein; 190 AA.

XX AAO18223;
AC AAO18223;
DT 18-SEP-2002 (first entry)
DE Human Bcl-Rambo BHNo domain related protein #4.
XX Human; apoptotic signal transduction protein; Bcl-Rambo; BHNo domain;
KW cancer; neurodegenerative disease; Alzheimer's disease; cytostatic;
KW neurotropic; neuroprotective; antiparkinsonian; virucide; antiinflammatory;
KW immunosuppressive; anti-HIV; antibacterial; hepatotropic; septic shock;
KW Parkinson's disease; muscular dystrophy; HIV; viral infection; hepatitis;
KW graft versus host disease; autoimmune disease.

XX Unidentified.
OS WO200248353-A2.
PN 20-JUN-2002.

XX 12-DEC-2001; 2001WO-EP14597.
XX 12-DEC-2000; 2000DE-1061766.
PR 04-JAN-2001; 2001DE-1000280.

XX (APOT-) APOTECH RES & DEV LTD.
PA Techopp J, Hofmann K;
XX WPI; 2002-537627/57.

XX New DNA encoding Bcl-Rambo protein, useful for treating e.g. tumors and
PT for identifying therapeutic modulators of Bcl-Rambo function -
XX Disclosure; Fig 1; 61pp; German.

XX The present invention provides the protein and coding sequences of the
CC human Bcl-Rambo apoptotic transcription factor, particularly the BHNo
CC domain. The sequences are useful in the treatment of diseases caused by
CC incorrectly regulated intracellular signal transduction, including
CC cancers, neurodegenerative diseases (e.g. Alzheimer's or Parkinson's
CC diseases), muscular dystrophy, viral infections (including human
CC immunodeficiency virus), autoimmune disease, septic shock, graft versus
CC host disease and acute hepatitis. The present sequence is a protein
CC described in the exemplification of the invention.

XX SQ Sequence 190 AA;
Query Match 81.6%; Score 821.5; DB 23; Length 190;
Best Local Similarity 88.1%; Pred. NC. 1.2e-82;
Matches 170; Conservative 0; Mismatches 20; Indels 3; Gaps 3;

QY 1 MATPASAPDTRALVADPVGYKLRQKGVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASAPXTXAXVAD-XGYKLRQKGVYVNGAGPGXGPAAD-XHQXRAAGXEFETRFRRT 58
QY 61 FSDLAQLHVTGPSAQORFTQVSDELFOGPGNWRGLVAFVFGAALCAESVKNEMEPLVG 120
DB 59 FSDLAQLHVTGPSAQORFTQVSDELFOGPGNWRGXAXAFVFGAAXCAESVKNEMEPLVG 118
QY 121 QVQEWVAYLETRADWIHSSGGWAEFTALYGDGALEEARLRREGNWA5RTVLTGAVAL 180
DB 119 QVQEWVAYLETXLAX-IHSSGGWAEFTALYGDGALEEARLRREGNWA5RTVLTGAVAL 177

QY 181 GALVTVGAFPAASK 193
DB 178 GALVTVGAFPAASK 190

RESULT 14
AAW59884
ID AAW59884 standard; Protein; 365 AA.

XX AAW59884;
AC AAW59884;
DT 20-NOV-1998 (first entry)
DE Amino acid sequence of the cDNA clone Bcl-like (HAICH29).
XX Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
KW immunological disorder; autoimmune disease; anti-infectious agent.

XX Homo sapiens.
XX WO9831800-A2.
XX 23-JUL-1998.

XX 21-JAN-1998; 98WO-US00960.
XX 21-JAN-1997; 97US-0034205.
PR 21-JAN-1997; 97US-0034204.
XX (AUCK-) AUCKLAND UNISERVICES LTD.
XX (HUMA-) HUMAN GENOME SCI INC.

XX Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA;
XX Su JY;
XX WPI; 1998-414099/35.
DR N-PSDB; AAV41925.

XX New isolated polynucleotides and encoded polypeptides - used to
PT develop products for treating e.g. inflammatory diseases,
PT infections, immunological disorders, autoimmune diseases, allergies
PT or tumours

XX Claim 1; Fig 12A-12D; 120pp; English.

XX This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29),
CC used in the method of the invention. The products of the clone can be
CC used for treating conditions associated with abnormal expression of
CC the polypeptides. They can be used for e.g. treating chronic
CC inflammatory diseases, immunological disorders, autoimmune diseases,
CC inflammatory diseases, various allergies, and as anti-infectious agents.
CC The products can also be used for detection and diagnosis.

XX SQ Sequence 365 AA;

Query Match 76.1%; Score 766; DB 19; Length 365;
Best Local Similarity 100.0%; Pred. No. 4.1e-76;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPVGYKLRQKGVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASAPDTRALVADPVGYKLRQKGVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHVTGPSAQORFTQVSDELFOGPGNWRGLVAFVFGAALCAESVKNEMEPLVG 120
DB 61 FSDLAQLHVTGPSAQORFTQVSDELFOGPGNWRGLVAFVFGAALCAESVKNEMEPLVG 120
QY 121 QVQEWVAYLETRADWIHSSGGW 144
DB 121 QVQEWVAYLETRADWIHSSGGW 144

RESULT 15

ABG95556
ID ABG95556 standard; Protein; 365 AA.
XX AC
XX ABG95556;
XX
DT 15-JAN-2003 (first entry)
XX
XX Human novel secreted protein gene 120 polypeptide #1.
XX
XX Human; secreted protein; autoimmune disease; chemoraxis;
KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasia;
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
KW nervous system disorder; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; tissue regeneration;
KW epithelial cell proliferation; organ transplantation; food additive;
KW preservative; nutritional.
XX
XX CS Homo sapiens.
XX
XX US6420526-B1.
XX
XX 16-JUL-2002.
XX
XX 08-SEP-1998; 98US-0149476.
XX
XX 07-MAR-1997; 97US-038621P.
XX 07-MAR-1997; 97US-040161P.
XX 07-MAR-1997; 97US-040162P.
XX 07-MAR-1997; 97US-040163P.
XX 07-MAR-1997; 97US-040333P.
XX 07-MAR-1997; 97US-040334P.
XX 07-MAR-1997; 97US-040336P.
XX 07-MAR-1997; 97US-040626P.
XX 11-APR-1997; 97US-043311P.
XX 11-APR-1997; 97US-043312P.
XX 11-APR-1997; 97US-043313P.
XX 11-APR-1997; 97US-043314P.
XX 11-APR-1997; 97US-043315P.
XX 11-APR-1997; 97US-043368P.
XX 11-APR-1997; 97US-043569P.
XX 11-APR-1997; 97US-043576P.
XX 11-APR-1997; 97US-043578P.
XX 11-APR-1997; 97US-043580P.
XX 11-APR-1997; 97US-043669P.
XX 11-APR-1997; 97US-043670P.
XX 11-APR-1997; 97US-043671P.
XX 11-APR-1997; 97US-043672P.
XX 11-APR-1997; 97US-043674P.
XX 23-MAY-1997; 97US-047492P.
XX 23-MAY-1997; 97US-047500P.
XX 23-MAY-1997; 97US-047501P.
XX 23-MAY-1997; 97US-047502P.
XX 23-MAY-1997; 97US-047503P.
XX 23-MAY-1997; 97US-047581P.
XX 23-MAY-1997; 97US-047582P.
XX 23-MAY-1997; 97US-047583P.
XX 23-MAY-1997; 97US-047584P.
XX 23-MAY-1997; 97US-047585P.
XX 23-MAY-1997; 97US-047586P.
XX 23-MAY-1997; 97US-047587P.
XX 23-MAY-1997; 97US-047588P.
XX 23-MAY-1997; 97US-047589P.
XX 23-MAY-1997; 97US-047590P.
XX 23-MAY-1997; 97US-047592P.
XX 23-MAY-1997; 97US-047593P.
XX 23-MAY-1997; 97US-047594P.
XX 23-MAY-1997; 97US-047595P.
XX 23-MAY-1997; 97US-047596P.
XX 23-MAY-1997; 97US-047597P.
XX 23-MAY-1997; 97US-047598P.
XX 23-MAY-1997; 97US-047599P.
XX 23-MAY-1997; 97US-047600P.
PR 23-MAY-1997; 97US-047601P.
PR 23-MAY-1997; 97US-047612P.
PR 23-MAY-1997; 97US-047613P.
PR 23-MAY-1997; 97US-047614P.
PR 23-MAY-1997; 97US-047615P.
PR 23-MAY-1997; 97US-047617P.
PR 23-MAY-1997; 97US-047618P.
PR 23-MAY-1997; 97US-047632P.
PR 23-MAY-1997; 97US-047633P.
PR 06-JUN-1997; 97US-048964P.
PR 06-JUN-1997; 97US-048974P.
PR 13-JUN-1997; 97US-049610P.
PR 08-JUL-1997; 97US-051926P.
PR 16-JUL-1997; 97US-052874P.
PR 18-AUG-1997; 97US-055724P.
PR 22-AUG-1997; 97US-056630P.
PR 22-AUG-1997; 97US-056631P.
PR 22-AUG-1997; 97US-056632P.
PR 22-AUG-1997; 97US-056636P.
PR 22-AUG-1997; 97US-056637P.
PR 22-AUG-1997; 97US-056662P.
PR 22-AUG-1997; 97US-056664P.
PR 22-AUG-1997; 97US-056822P.
PR 22-AUG-1997; 97US-056864P.
PR 22-AUG-1997; 97US-056872P.
PR 22-AUG-1997; 97US-056874P.
PR 22-AUG-1997; 97US-056875P.
PR 22-AUG-1997; 97US-056876P.
PR 22-AUG-1997; 97US-056877P.
PR 22-AUG-1997; 97US-056878P.
PR 22-AUG-1997; 97US-056879P.
PR 22-AUG-1997; 97US-056880P.
PR 22-AUG-1997; 97US-056881P.
PR 22-AUG-1997; 97US-056882P.
PR 22-AUG-1997; 97US-056884P.
PR 22-AUG-1997; 97US-056886P.
PR 22-AUG-1997; 97US-056887P.
PR 22-AUG-1997; 97US-056888P.
PR 22-AUG-1997; 97US-056889P.
PR 22-AUG-1997; 97US-056892P.
PR 22-AUG-1997; 97US-056893P.
PR 22-AUG-1997; 97US-056894P.
PR 22-AUG-1997; 97US-056903P.
PR 22-AUG-1997; 97US-056908P.
PR 22-AUG-1997; 97US-056909P.
PR 22-AUG-1997; 97US-056910P.
PR 22-AUG-1997; 97US-056911P.
PR 22-AUG-1997; 97US-057761P.
PR 03-SEP-1997; 97US-057650P.
PR 03-SEP-1997; 97US-057669P.
PR 12-SEP-1997; 97US-058785P.
PR 06-MAR-1998; 97US-061060P.
XX 98WO-US04493.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruber SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarik DR;
XX Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
XX Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
XX Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX WPI; 2002-634796/68.
XX
XX New isolated human secreted protein for diagnosing, preventing,
XX treating or ameliorating medical conditions and used as a food additive
XX or preservative -
XX
XX Disclosure; Column 103; 129pp; English.
XX
XX The invention relates to an isolated protein that is one of 186 human
XX secreted proteins, given in the specification, encoded by one of
XX 309 cDNA sequences also given in the specification. The protein is used

CC in a pharmaceutical composition used to prevent, treat or ameliorate a
CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
CC dogs, chickens or sheep. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. The present sequence represents one of the novel human
CC secreted proteins of the invention..

XX
SQ Sequence 365 AA;

Query Match 76.1%; Score 766; DB 23; Length 365;
Best Local Similarity 100.0%; Pred. No. 4.1e-76;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATPASAPDTRALVADFVGYKLROKGYVCGAGPGGPAADPLHQAMRAAGDEFFETRFRRT 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MATPASAPDTRALVADFVGYKLROKGYVCGAGPGGPAADPLHQAMRAAGDEFFETRFRRT 60
QY 61 FSDLAQLHVTFGSAQQRFTQVSDLEFQGGPNWGRIVAFVFGAALCAESVKNEMEPLVG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 FSDLAQLHVTFGSAQQRFTQVSDLEFQGGPNWGRIVAFVFGAALCAESVKNEMEPLVG 120
QY 121 QVQENMVAYLETRLADWIHSSGGW 144
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 QVQENMVAYLETRLADWIHSSGGW 144

Search completed: October 24, 2003, 10:48:54
Job time : 63 secs

1	1002	99.5	193	1	US-08-758-897-4	Sequence 4, Appli
2	1002	99.5	193	2	US-08-978-523-4	Sequence 4, Appli
3	997	99.0	192	1	US-08-798-897-6	Sequence 6, Appli
4	997	99.0	192	2	US-08-578-523-6	Sequence 6, Appli
5	996	98.9	193	1	US-08-798-897-3	Sequence 3, Appli
6	996	98.9	193	2	US-08-578-523-3	Sequence 3, Appli
7	991	98.4	192	1	US-08-798-897-5	Sequence 5, App-
8	991	98.4	192	2	US-08-978-523-5	Sequence 5, App-
9	766	76.1	365	4	US-09-149-476-696	Sequence 696, App
10	429.5	42.7	233	4	US-09-271-014-A-6	Sequence 6, Appli
11	428.5	42.6	233	1	US-08-333-565-59	Sequence 59, Appl
12	428.5	42.6	233	1	US-08-081-448-6	Sequence 6, Appli
13	428.5	42.6	233	1	US-08-607-369-24	Sequence 24, Appl
14	428.5	42.6	233	1	US-08-471-058-14	Sequence -14, Appl
15	428.5	42.6	233	2	US-08-661-479-59	Sequence 59, Appl
16	428.5	42.6	233	2	US-08-470-670A-7	Sequence 7, Appli
17	428.5	42.6	233	3	US-08-471-057-14	Sequence 14, Appl
18	428.5	42.6	233	3	US-08-481-739-2	Sequence 2, Appli
19	428.5	42.6	233	3	US-09-167-921-2	Sequence 2, Appli
20	428.5	42.6	233	3	US-09-323-743-2	Sequence 2, Appli
21	428.5	42.6	233	4	US-08-461-511A-7	Sequence 7, Appli
22	428.5	42.6	233	4	US-08-470-865-14	Sequence 14, Appli
23	428.5	42.6	233	5	PCT-US94-07089-7	Sequence 7, Appli
24	428.5	42.6	233	5	PCT-US95-04600-24	Sequence 24, Appl
25	425	42.2	225	3	US-09-101-519-1	Sequence 1, Appli
26	423.5	42.1	233	5	US-08-607-369-23	Sequence 23, Appl
27	423.5	42.1	233	5	PCT-US95-04600-23	Sequence 23, Appl

Db 61 FSDLAQLHVTGPSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120
QY 121 QVQEMWVAYLETRLDWIHSSGGWAEFTALYDGALEEAARRLRREGNWSVRTVLTGAVAL 180
Db 121 QVQEMWVAYLETRLDWIHSSGGWAEFTALYDGALEEAARRLRREGNWSVRTVLTGAVAL 180
QY 181 GALVTVGAFPAASK 193
Db 181 GALVTVGAFPAASK 193

RESULT 2

US-08-978-523-4
; Sequence 4, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.3, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-978-523-4

Query Match 99.5%; Score 1002; DB 2; Length 193;
Best Local Similarity 99.5%; Pred. No. 6.9e-107;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
Db 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHVTGPSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120
Db 61 FSDLAQLHVTGPSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120
QY 121 QVQEMWVAYLETRLDWIHSSGGWAEFTALYDGALEEAARRLRREGNWSVRTVLTGAVAL 180
Db 121 QVQEMWVAYLETRLDWIHSSGGWAEFTALYDGALEEAARRLRREGNWSVRTVLTGAVAL 180

QY 181 GALVTVGAFPAASK 193
Db 181 GALVTVGAFPAASK 193
RESULT 3
US-08-798-897-6
; Sequence 6, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-798-897-6

Query Match 99.0%; Score 997; DB 1; Length 192;
Best Local Similarity 99.5%; Pred. No. 2.6e-106;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATPASAPDTRALVADPVGYKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRTF 61
Db 1 ATPASAPDTRALVADPVGYKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRTF 60
QY 62 SDLAALHVTGPSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQ 121
Db 61 SDLAALHVTGPSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQ 120
QY 122 VQEMWVAYLETRLDWIHSSGGWAEFTALYDGALEEAARRLRREGNWSVRTVLTGAVALG 181
Db 121 VQEMWVAYLETRLDWIHSSGGWAEFTALYDGALEEAARRLRREGNWSVRTVLTGAVALG 180
QY 182 ALVTVGAFPAASK 193
Db 181 ALVTVGAFPAASK 192

RESULT 4

US-08-978-523-6
; Sequence 6, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John

;; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
;; TITLE OF INVENTION: Homologue
;; NUMBER OF SEQUENCES: 53
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;; STREET: 1100 New York Avenue, N.W., Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/978,523
;; FILING DATE: herewith
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/798,897
;; FILING DATE: February 11, 1997
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Esmond, Robert W.
;; REGISTRATION NUMBER: 32,893
;; REFERENCE/DOCKET NUMBER: 1483.0140002
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 192 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-978-523-6
Query Match 99.0%; Score 997; DB 2; Length 192;
Best Local Similarity 99.5%; Pred. No. 2.6e-106;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATPASAPDTRALVADVFYGYKLRQKGYVCGAGGEGPAADPLHQAAMRAAGDEFEETRFRRT 61
DB 1 ATPASAPDTRALVADVFYGYKLRQKGYVCGAGGEGPAADPLHQAAMRAAGDEFEETRFRRT 60
QY 62 SDLAALQHLVTPGSAQQRFTQVSDLELFOGGPNWGRLVAFVFGAALCAESVKNKEPELVGQ 121
DB 61 SDLAALQHLVTPGSAQQRFTQVSDLELFOGGPNWGRLVAFVFGAALCAESVKNKEPELVGQ 120
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DB 121 VQEWVAYLETRLADWIHSSGGWAEFTALYGDGCALEEARLRREGNWSVTVLTGVALG 180
QY 182 ALVTVGAFASK 193
DB 181 ALVTVGAFASK 192

RESULT 5
US-08-978-897-3
; Sequence 3, Application US/08/798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington

;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/798,897
;; FILING DATE: February 11, 1997
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Esmond, Robert W.
;; REGISTRATION NUMBER: 32,893
;; REFERENCE/DOCKET NUMBER: 1483.0140001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 193 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-798-897-3
Query Match 98.9%; Score 996; DB 1; Length 193;
Best Local Similarity 98.4%; Pred. No. 3.4e-106;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADVFYGYKLRQKGYVCGAGGEGPAADPLHQAAMRAAGDEFEETRFRRT 60
DB 1 MATPASAPDTRALVADVFYGYKLRQKGYVCGAGGEGPAADPLHQAAMRAAGDEFEETRFRRT 60
QY 61 FSDLAALQHLVTPGSAQQRFTQVSDLELFOGGPNWGRLVAFVFGAALCAESVKNKEPELVG 120
DB 61 FSDLAALQHLVTPGSAQQRFTQVSDLELFOGGPNWGRLVAFVFGAALCAESVKNKEPELVG 120
QY 121 VQEWVAYLETRLADWIHSSGGWAEFTALYGDGCALEEARLRREGNWSVTVLTGVAL 180
DB 121 VQEWVAYLETRLADWIHSSGGWAEFTALYGDGCALEEARLRREGNWSVTVLTGVAL 180
QY 181 GALVTVGAFASK 193
DB 181 GALVTVGAFASK 193

RESULT 6
US-08-978-523-3
; Sequence 3, Application US/08/78523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith

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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-798-897-5

Query Match          98.9%; Score 996; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 3.4e-106;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADVGVGKLRQKGVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASPTDTRALVADVGVGKLRQKGVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSLAAQLHVTGSAQORFTQVSDQLFQGGPNMGRVLAFFVFGAALCAESVKNEMEPLVG 120
DB 61 FSLAAQLHVTGSAQORFTQVSDQLFQGGPNMGRVLAFFVFGAALCAESVKNEMEPLVG 120
QY 121 QVQEMVAYLETRLADWIHSSGGAETALYGDGALEEARLRREGNWSVRTVLTGAVAL 180
DB 121 QVQDMVYTLERLADWIHSSGGAETALYGDGALEEARLRREGNWSVRTVLTGAVAL 180
QY 181 GALVTUGAFFASK 193
DB 181 GALVTUGAFFASK 193

RESULT 7
US-08-798-897-5
; Sequence 5, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600

```

```

; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-798-897-5

Query Match          98.4%; Score 991; DB 1; Length 192;
Best Local Similarity 98.4%; Pred. No. 1.2e-105;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATPASAPDTRALVADVGVGKLRQKGVCGAGGEGPAADPLHQAMRAAGDEFETRFRRTF 61
DB 1 ATPASTPTDTRALVADVGVGKLRQKGVCGAGGEGPAADPLHQAMRAAGDEFETRFRRTF 60
QY 62 SDLAAQLHVTGSAQORFTQVSDQLFQGGPNMGRVLAFFVFGAALCAESVKNEMEPLVGQ 121
DB 61 SDLAAQLHVTGSAQORFTQVSDQLFQGGPNMGRVLAFFVFGAALCAESVKNEMEPLVGQ 120
QY 122 QVQEMVAYLETRLADWIHSSGGAETALYGDGALEEARLRREGNWSVRTVLTGAVALG 181
DB 121 QVQDMVYTLERLADWIHSSGGAETALYGDGALEEARLRREGNWSVRTVLTGAVALG 180
QY 182 ALVTUGAFFASK 193
DB 181 ALVTUGAFFASK 192

RESULT 8
US-08-978-523-5
; Sequence 5, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-08-978-523-5
Query Match: 98.4%; Score 991; DB 2; Length 192;
Best Local Similarity 98.4%; Pred. No. 1.2e-105;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATPASADTALVADFVGYKLROKGYVCGAGPQGGPAADPLHQMRAAGDEFTTRPTTF 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATPASTDTALVADFVGYKLROKGYVCGAGPQGGPAADPLHQMRAAGDEFTTRPTTF 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 62 SDLAALQHVTPGSAQQFTQVSDELFOGPNMGRVLVAFFVFGAALCAESVNKEMEPVLVGQ 121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 SDLAALQHVTPGSAQQFTQVSDELFOGPNMGRVLVAFFVFGAALCAESVNKEMEPVLVGQ 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 122 VQEMVAYLETRLADWTHSSGGMAEFTALYGDGALEEARLRREGNWSVRTVLTGVALG 181
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 VQDMVTYLETRLADWTHSSGGMAEFTALYGDGALEEARLRREGNWSVRTVLTGVALG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 182 ALVTGGAFFASK 193
    ||||| ||||| |||||
Db 181 ALVTGGAFFASK 192
    ||||| ||||| |||||

RESULT 9
US-09-149-476-696
; Sequence 696, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,936
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match      76.1%; Score 766; DB 4; Length 365;
Best Local Similarity 100.0%; Pred. No. 2e-79;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MATASAPDTRALVADFVGYKLROKGYVCGAGPGEPAADPLHOAMRAAGDEFETRFRPT 60
      |||
Db      1 MATASAPDTRALVADFVGYKLROKGYVCGAGPGEPAADPLHOAMRAAGDEFETRFRPT 60
      |||

QY      61 FSDLAALQHLVTPGSAQORFTQVSDLFQGGPNWRLVAFVFGAALCAESVKNKEPLVG 120
      |||
Db      61 FSDLAALQHLVTPGSAQORFTQVSDLFQGGPNWRLVAFVFGAALCAESVKNKEPLVG 120
      |||

QY      121 QVQEMWVAYLETRLADWIHSSGGW 144
      |||
Db      121 QVQEMWVAYLETRLADWIHSSGGW 144
      |||

RESULT 10
US-09-271-014A-6
; Sequence 6, Application US/09271014A
; Patent No. 6395510
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, CRAIG B.
; APPLICANT: BOISE, LAWRENCE H.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:316
; CURRENT APPLICATION NUMBER: US/09/271.014A
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Human
JS-09-271-014A-6

Query Match      42.7%; Score 429.5; DB 4; Length 233;
Best Local Similarity 41.1%; Pred. No. 3.9e-41;
Matches 92; Conservative 23; Mismatches 58; Indels 51; Gaps 4;

QY      11 RALVADFVGYKLROKGYVC-----GAGP-----GEGPAA 39
      |||
Db      6 RELVDFLSYKLSOKGYSWQSQFSDVENRTEAPGTGSEMTPTSAINGNPWHLADSPAV 65
      |||

QY      40 D-----PLHQAMRAAGDEFETRFRPTFSDLAALQHLVTPGSAQORFTQ 81
      |||
Db      66 NGATAHSSSLDAREVIPAAVKQALREAGDDEFELRYRPAFSDJTSQHLITPGTAYQSEFQ 125
      |||

QY      82 VSDLFQGGPNWRLVAFVFGAALCAESVKNKEPLVGQVQEMWVAYLETRLADWIHSS 141
      |||
Db      126 VYNELFRDGVNWRIVAFVFGGALCVESVDKEXQVLVSRIAAMWATYINDHLEPFIQEN 185
      |||

QY      142 GWAEFTALYGDGALEBARLRE--GNWASVRTVLGTGVALGAL 183
      |||
Db      186 GWDTFVELYGNNAAESRKQERFNWFLTGMTVAGVVLLGSL 229
      |||

RESULT 11
US-08-333-565-59
; Sequence 59, Application US/08333565
; Patent No. 5622852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
```

```
;
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,565
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-333-565-59

Query Match 42.6%; Score 428.5; DB 1; Length 233;
Best Local Similarity 41.3%; Pred. No. 5.1e-41;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADFVGYKLRQGY-----V 28
Db 6 RELVVDFLSYKLSQKYSWQSFSDVEENRTEAPEGTSEMETPSAINGNPSWHLADSPAV 65
QY 29 CGAGPGEGPAD-----PLHQXRAAGDEFEFRTRFTSDLAQLHVTGSAOQRT 80
Db 66 NGA-TGHSSLDAREV-PMAAVKQALREAGDEFELRYRRAFSDLTSLHITPGTAQSFE 124
QY 81 QVSEDLFGGPNWGRVAVFFVFGAALCAESVNKMEPLVQGVQVEMVAYLETRLADWHS 140
Db 125 QVNNELFRDGVNMGRIVAFESFGGALCVESVDKEMQVLVSRIAAMWATYLNHLEPWIQ 194
QY 141 SGWAEFTALYGDGCALEARRLE--GNWASVRTVLTGVALGAL 183
Db 185 NGGMDTFVELYGNNAABESRKQERFNRWFLTGMTVAGVVLGSL 229

RESULT 12
; US-08-081-448-6
; Sequence 6, Application US/08081448
; Patent No. 5646008
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5646008th Clark Street, Suite 800
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,448
; FILING DATE: 19930622
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646008thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-744-0090
; TELEFAX: 312-755-4489
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-081-448-6

Query Match 42.6%; Score 428.5; DB 1; Length 233;
Best Local Similarity 40.6%; Pred. No. 5.1e-41;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADFVGYKLRQGY-----VCGASP-----GEGPAA 39
Db 6 RELVVDFLSYKLSQKYSWQSFSDVEENRTEAPEGTSEMETPSAINGNPSWHLADSPAV 65
QY 40 D-----PLHQXRAAGDEFEFRTRFTSDLAQLHVTGSAOQRTQ 81
Db 66 NGATAHSSLDAREV-PMAAVKQALREAGDEFELRYRRAFSDLTSLHITPGTAQSFEQ 125
QY 82 VSEDLFGGPNWGRVAVFFVFGAALCAESVNKMEPLVQGVQVEMVAYLETRLADWHS 141
Db 126 VVNNELFRDGVNMGRIVAFESFGGALCVESVDKEMQVLVSRIAAMWATYLNHLEPWIQ 185
QY 142 GSWAEFTALYGDGCALEARRLE--GNWASVRTVLTGVALGAL 183
Db 186 GGMWDTFVELYGNNAABESRKQERFNRWFLTGMTVAGVVLGSL 229

RESULT 13
; US-08-607-269-24
; Sequence 24, Application US/08607269
; Patent No. 5702897
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: Interaction of Proteins Involved in a
; TITLE OF INVENTION: Cell Death Pathway
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/607,269
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/226,876
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
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; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-607-269-24

Query Match 42.6%; Score 428.5; DB 1; Length 233;
Best Local Similarity 40.6%; Pred. No. 5.1e-41;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADPVGKLRQKGY-----VCGAGP-----GEGPAA 39
Db 6 RELVVDLSYLSQKGYSWQFSDVEENRTEAPGTESEMETPSAINGNPSWHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFETFRRTFSDLAQLHVTPTGSAQQRFTQ 81
Db 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPTGTAYQSFQ 125
QY 82 VSDLEFGGPNWGRVAVFFVFGAALCAESYNKEMEPLVGVQVQWVAYLETRLADMIHS 141
Db 126 VVNELFRDGVNMGRIVAVFFSFGGALCVESVDKEMQVLVSRIAAMATYLNHLEPIQEN 185
QY 142 GGNAEFTALYCGGALAEARLR--GNWASVRTVLTGAVALGAL 183
Db 186 GGWDTFVELYGNNAAESRKQGRFNRFLTGMTVAGVLLGSJ 229

RESULT 14
US-08-471-058-14
; Sequence 14, Application US/0847:058
; Patent No. 5770443
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Bart, Philip J.
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
; TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; APPLICATION NUMBER: 08/160,067
; FILING DATE: 30-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792

; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-607-269-24

Query Match 42.6%; Score 428.5; DB 1; Length 233;
Best Local Similarity 40.6%; Pred. No. 5.1e-41;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADPVGKLRQKGY-----VCGAGP-----GEGPAA 39
Db 6 RELVVDLSYLSQKGYSWQFSDVEENRTEAPGTESEMETPSAINGNPSWHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFETFRRTFSDLAQLHVTPTGSAQQRFTQ 81
Db 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPTGTAYQSFQ 125
QY 82 VSDLEFGGPNWGRVAVFFVFGAALCAESYNKEMEPLVGVQVQWVAYLETRLADMIHS 141
Db 126 VVNELFRDGVNMGRIVAVFFSFGGALCVESVDKEMQVLVSRIAAMATYLNHLEPIQEN 185
QY 142 GGNAEFTALYCGGALAEARLR--GNWASVRTVLTGAVALGAL 183
Db 186 GGWDTFVELYGNNAAESRKQGRFNRFLTGMTVAGVLLGSJ 229

RESULT 15
US-08-661-479-59
; Sequence 59, Application: US/08661479
; Patent No. 5834209
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,479
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,565
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-661-479-59
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Query Match 42.6%; Score 428.5; DB 2; Length 233;
Best Local Similarity 41.3%; Pred. No. 5.1e-41;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;
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DB 66 NGA-TGHSLSLDAREVIPMAAVKQA-REAGDEPELRYRRAFSDLTSQLHITPTAYQSF 124
QY 81 QVSDLELFGGPNMGRLVAFVFGAALCAESVNKEMEPFLVGQVQEMWVAYLETRLADWZHS 140
DB 125 QVYNELFRDGVNMGRIVAFVFGGALCVESVDKEMQVLVSRIAAMWATYLNCHLEPWIOE 184
QY 141 SGGWAEFTALYGDGALAEERLRE--GNWASVRTVLTGVALGAL 183
DB 185 NGGWDTFVELYGNNAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229

Search completed: October 24, 2003, 10:52:51
Job time : 23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 24, 2003, 10:51:15 ; Search time 45.5 Seconds

(without alignments)
710.328 Million cell updates/sec

Title: US-09-925-674A-7

Perfect score: 1007

Sequence: 1 MATPASADPTALVADFGV.....LTGAVALGALVTVGAPFASK 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1007	100.0	193	10	US-09-925-674A-7
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3	766	76.1	365	11	US-09-809-391-696
4	766	76.1	365	12	US-09-882-171-696
5	428.5	42.6	233	9	US-09-734-846-2
6	428.5	42.6	233	10	US-09-952-278-6
7	428.5	42.6	233	12	US-10-169-223-10
8	428.5	42.6	233	12	US-10-302-262-2
9	428.5	42.6	233	15	US-10-101-482-14
10	428.5	42.6	233	15	US-10-072-830-4
11	415.5	41.3	152	15	US-10-158-769-2
12	412.5	41.0	239	15	US-10-277-693A-10
13	410.5	40.8	239	8	US-08-726-211-5
14	410.5	40.8	239	12	US-10-141-618-12
15	410.5	40.8	239	12	US-10-053-645A-21

16	410.5	40.8	239	15	US-10-101-482-12	Sequence 12, Appl
17	410.5	40.8	239	15	US-10-072-830-2	Sequence 2, Appl
18	406	40.3	236	15	US-10-277-693A-11	Sequence 11, Appl
19	401	39.8	212	12	US-10-169-223-14	Sequence 14, Appl
20	378	37.5	190	10	US-09-952-278-2	Sequence 2, Appl
21	374.5	37.2	235	15	US-10-208-155-2	Sequence 2, Appl
22	374	37.1	155	15	US-10-158-769-1	Sequence 1, Appl
23	373.5	37.1	185	9	US-09-864-761-40954	Sequence 40954, A
24	346	34.4	205	8	US-08-726-211-7	Sequence 7, Appl
25	346	34.4	205	10	US-09-952-278-4	Sequence 4, Appl
26	346	34.4	205	12	US-10-053-645A-23	Sequence 23, Appl
27	241	23.9	49	9	US-09-864-761-34213	Sequence 34213, A
28	205	20.4	63	10	US-09-952-278-3	Sequence 3, Appl
29	183	18.2	170	10	US-09-952-278-8	Sequence 8, Appl
30	176	17.5	211	15	US-10-101-482-7	Sequence 7, Appl
31	176	17.5	211	15	US-10-101-482-10	Sequence 10, Appl
32	176	17.5	211	15	US-10-189-294-2	Sequence 2, Appl
33	176	17.5	211	15	US-10-177-293-25	Sequence 25, Appl
34	173	17.2	211	15	US-10-101-482-9	Sequence 9, Appl
35	173	17.2	211	15	US-10-101-482-11	Sequence 11, Appl
36	168.5	16.7	210	15	US-10-101-482-22	Sequence 22, Appl
37	155.5	15.4	192	15	US-10-277-693A-8	Sequence 46, Appl
38	153	15.2	191	15	US-10-196-793A-46	Sequence 5, Appl
39	153	15.2	192	12	US-10-306-878-5	Sequence 13, Appl
40	153	15.2	192	15	US-10-101-482-13	Sequence 9, Appl
41	153	15.2	192	15	US-10-277-693A-9	Sequence 2, Appl
42	153	15.2	331	9	US-09-033-525-2	Sequence 19, Appl
43	152	15.1	192	15	US-10-277-693A-2	Sequence 0, Appl
44	150	14.9	280	15	US-10-101-482-19	
45	149	14.8	117	15	US-10-189-294-4	

ALIGNMENTS

RESULT 1

US-09-925-674A-7
; Sequence 7, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; FILE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: P88965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 193
; TYPE: PRT
; ORGANISM: HUMAN
US-09-925-674A-7

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Best Local Similarity:	100.0%;	Pred. No.	3.9e-102;				
Matches	193;	Conservative	0;	Mismatches	0;	Gaps	0;
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Db	1	MATPASADPTALVADFGVYKLRQYVCGAGPGEPAADPLHOAMRAAGDEFTFRRT	60				
QY	61	FSDLAALQHVTPGSAQORFTQVSDLEFGGPNWRLVAFVFGAALCAESVYKMEPLVG	120				
Db	61	FSDLAALQHVTPGSAQORFTQVSDLEFGGPNWRLVAFVFGAALCAESVYKMEPLVG	120				
QY	121	QVQEMWVAYLETRLADMTIHSSGGWAEFTALYGDGALBEARLRGNWASVRTVLITGAVAL	180				
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Db      181  GALVTVGAFASK 193

RESULT 2
US-09-925-674A-9
; Sequence 9, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: P88965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mouse
US-09-925-674A-9

Query Match      99.0%; Score 997; DB 10; Length 193;
Best Local Similarity 98.4%; Pred. No. 4.9e-101;
Matches 190; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      121 QVQEMMVAYLETRLADWIHSSGGW 144
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Db      121 QVQEMMVAYLETRLADWIHSSGGW 144

RESULT 4
US-09-882-171-696
; Sequence 696, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
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; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
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; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23

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Db      181  GALVTVGAFASK 193

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Best Local Similarity 100.0%; Pred. No. 2.3e-75;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-09-809-391-696
; Sequence 696, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 696
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-391-696
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2 PRIOR FILING DATE: 1997-05-23
3 PRIOR APPLICATION NUMBER: 60/047,613
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5 PRIOR APPLICATION NUMBER: 60/047,582
6 PRIOR FILING DATE: 1997-05-23
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8 PRIOR FILING DATE: 1997-05-23
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10 PRIOR FILING DATE: 1997-05-23
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14 PRIOR FILING DATE: 1997-05-23
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88 PRIOR FILING DATE: 1997-08-22
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95 PRIOR APPLICATION NUMBER: 60/047,585
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97 PRIOR APPLICATION NUMBER: 60/047,586
98 PRIOR FILING DATE: 1997-05-23
99 PRIOR APPLICATION NUMBER: 60/047,590
100 PRIOR FILING DATE: 1997-05-23
101 PRIOR APPLICATION NUMBER: 60/047,594
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103 PRIOR APPLICATION NUMBER: 60/047,589
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105 PRIOR APPLICATION NUMBER: 60/047,593
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115 PRIOR APPLICATION NUMBER: 60/043,670
116 PRIOR FILING DATE: 1997-04-11
117 PRIOR APPLICATION NUMBER: 60/056,632
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131 PRIOR APPLICATION NUMBER: 60/056,897
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133 PRIOR APPLICATION NUMBER: 60/056,908
134 PRIOR FILING DATE: 1997-08-22
135 PRIOR APPLICATION NUMBER: 60/048,964
136 PRIOR FILING DATE: 1997-06-06
137 PRIOR APPLICATION NUMBER: 60/057,650
138 PRIOR FILING DATE: 1997-09-05
139 PRIOR APPLICATION NUMBER: 60/056,884
140 PRIOR FILING DATE: 1997-08-22
141 PRIOR APPLICATION NUMBER: 60/057,669
142 PRIOR FILING DATE: 1997-09-05

Query Match 76.1%; Score 766; DB 12; Length 365;
Best Local Similarity 100.0%; Pred.No. 2.3e-75;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 QVCEWVMVAYLETRLADWIHSSGGW 144
DB 121 QVCEWVMVAYLETRLADWIHSSGGW 144

RESULT 5
US-09-734-846-2
; Sequence 2, Application US/09734846
; Patent No. US20010007025A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0528
; CURRENT APPLICATION NUMBER: US/09/734,846
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/323,743
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-734-846-2

Query Match 42.6%; Score 428.5; DB 9; Length 233;
Best Local Similarity 40.6%; Pred. No. 1.2e-38;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADFVGVYKLRQKGY-----VCGAGP-----GEGPAA 39
DB 6 RELVDFLSYKLSQKGYSNQSFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFPETPRFRTRFSDLAQLHVTGPSAQORFTQ 81
DB 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLTHTPTAYQSFQ 125
QY 82 VSDELFOGPNWGRVAFVFGAALCAESVKNKEMEPLVGQVQEWVAYLETRLADWIHSS 141
DB 126 VVNELFDGNNWGRVAFVFGAALCAESVKNKEMEPLVGQVQEWVAYLETRLADWIHSS 185
QY 142 GGNAEFTALYGDGALEEARLRE--GNWASVRTVLTGAVALGAL 183
DB 186 GGMDFVELYGNNAAESRKGQERFNRWFLTGMTVAGVVLGSL 229

RESULT 6
US-09-952-278-6
; Sequence 6, Application US/09952278
; Patent No. US20020137182A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; Compositions and Methods
; NUMBER OF SEQUENCES: 8
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. US20020137182A1th Clark Street, Suite 800
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60610
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/952,278
; FILING DATE: 12-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,448
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020137182A1thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD09C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-744-0090
; TELEFAX: 312-755-4489
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-952-278-6

Query Match 42.6%; Score 428.5; DB 10; Length 233;
Best Local Similarity 40.6%; Pred. No. 1.2e-38;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADFVGVYKLRQKGY-----VCGAGP-----GEGPAA 39
DB 6 RELVDFLSYKLSQKGYSNQSFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFPETPRFRTRFSDLAQLHVTGPSAQORFTQ 81
DB 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLTHTPTAYQSFQ 125
QY 82 VSDELFOGPNWGRVAFVFGAALCAESVKNKEMEPLVGQVQEWVAYLETRLADWIHSS 141
DB 126 VVNELFDGNNWGRVAFVFGAALCAESVKNKEMEPLVGQVQEWVAYLETRLADWIHSS 185
QY 142 GGNAEFTALYGDGALEEARLRE--GNWASVRTVLTGAVALGAL 183
DB 186 GGMDFVELYGNNAAESRKGQERFNRWFLTGMTVAGVVLGSL 229

RESULT 7
US-10-169-223-10
; Sequence 10, Application US/10169223
; Publication No. US20030152946A1
; GENERAL INFORMATION:
; APPLICANT: SHIMIZU, Shigeomi
; APPLICANT: TSUJIMOTO, Yoshihide
; TITLE OF INVENTION: BH4-Fused Polypeptides
; FILE REFERENCE: 1422-0537P
; CURRENT APPLICATION NUMBER: US/10/169,223
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: JP 11-371449
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: PCT/JP00/09274
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.1
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US-10-072-830-4
; Sequence 4, Application US/10072830
; Publication No. US20030103945A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, DONG FENG
; APPLICANT: HUANG, XIZHONG
; APPLICANT: CHEN, GUANG
; APPLICANT: MANJI, HUSSEINI K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING AXON
; TITLE OF INVENTION: REGENERATION AND PREVENTING NEURONAL CELL DEGENERATION
; FILE REFERENCE: ERM-105.01
; CURRENT APPLICATION NUMBER: US/10/072.830
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/267,832
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/272,617
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/289,990
; PRIOR FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-830-4
Query Match 42.6%; Score 428.5; DB 15; Length 233;
Best Local Similarity 40.6%; Pred. No. 1.2e-36;
Matches 91; Conservative 23; Mismatches 55; Indels 51; Gaps 4;
QY 11 RALVADFVGYKLRQKGY-----PLHQAMRAAGDEFETRFRRTFSDLAALQHLVTPGSAQQRFTQ 39
DB 6 RELVDFLSYKLSQKGYMSQFSQSDVEENRTEAPEGTESEMEFELRYRRAFDLSLTSQHLITPGTAYQSFEQ 65
QY 40 D-----PLHQAMRAAGDEFETRFRRTFSDLAALQHLVTPGSAQQRFTQ 81
DB 66 NGATAHSSLDAREVIPAAYKQALREAGDEFELRYRRAFDLSLTSQHLITPGTAYQSFEQ 125
QY 82 VSDLFQGGPNWGRVAFVFGAALCAESVKNKEMPLVGVQVQVEMVAYLETRLAJWI 141
DB 126 VVNELPRDGVNMGRIYVAFVFGGALCVESVDKEMQVLVSRIAAMWATYLNHLEPWQIEN 185
QY 142 GQWAEPTALVCDGALAEARLRE--GNWASVRTVLTCAVALGAL 183
DB 186 GQWDTFVELYGNNAAESRKQGRFNRWFLTGMTVAGVLLGSL 229
RESULT 11
US-10-158-769-2
; Sequence 2, Application US/10158769
; Publication No. US20030008924A1
; GENERAL INFORMATION:
; APPLICANT: Weng, Shaoren
; APPLICANT: Yang, Dajun
; TITLE OF INVENTION: Small Molecule Antagonists of BCL-2 Family Protein
; FILE REFERENCE: UM-07232
; CURRENT APPLICATION NUMBER: US/10/158.769
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/293,983
; PRIOR FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-158-769-2
Query Match 41.3%; Score 415.5; DB 15; Length 152;
Best Local Similarity 53.0%; Pred. No. 1.7e-37;
Matches 80; Conservative 17; Mismatches 45; Indels 9; Gaps 1;
QY 11 RALVADFVGYKLRQKGYVCG-----AGFGGPAADPLHQAMRAAGDEFETRFRRTF 61
DB 2 RELVDFLSYKLSQKGYMSQFSQSDVEENRTEAPEGTESEAVKQALREAGDEFELRYRRAF 61
QY 62 SDLAALQHLVTPGSAQQRFTQVSDLFQGGPNWGRVAFVFGAALCAESVKNKEMPLVGVQ 121
DB 62 SLDLSQLHITGTAYQSFEQVYVNELPRDGVNMGRIYVAFVFGGALCVESVDKEMQVLVS 121
QY 122 VQEMVAYLETRLAJWIHSSGQWAEFTALYG 152
DB 122 IAAWMTYLNHLEPWQIENGWDTFVELYG 152
RESULT 12
US-10-277-693A-10
; Sequence 10, Application US/10277693A
; Publication No. US20030096367A1
; GENERAL INFORMATION:
; APPLICANT: Kormsmeier, Stanley J.
; TITLE OF INVENTION: Cell Death Agonists
; FILE REFERENCE: 56029/36280
; CURRENT APPLICATION NUMBER: US/10/277.693A
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/379,820
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 08/112,208
; PRIOR FILING DATE: 1993-08-26
; PRIOR APPLICATION NUMBER: 08/856,034
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-277-693A-10
Query Match 41.0%; Score 412.5; DB 15; Length 239;
Best Local Similarity 37.0%; Pred. No. 6.8e-37;
Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;
QY 9 DTRALVADFVGYKLRQKGYVCGAG-----PGE-----PGE----- 35
DB 1C DNREIVMKYIHYKLSQRYGWDAGDVGGAAPGGAAPAGPAGIFSSQPGRTPHPAASRDPVART 69
QY 36 -----GPAACP-----LHQAMRAAGDEFETRFRRTFSDLAALQHLVTPGSAQQR 78
DB 70 SPLQTPAAPGAANGPALSFPVPPVHLTLRQAGDDFSRYRDRDFAEMSSQLHLTPFTARGR 129
QY 79 FTQVSDLFQGGPNWGRVAFVFGAALCAESVKNKEMPLVGVQVQVEMVAYLETRLAJWI 138
DB 130 FATVVEELFRDGVNMGRIYVAFVFGGVMCVESVNRMSPLVDNIALMWTLYNRLHWTI 189
QY 139 HSSGQWAEFTALYGDALEEARLREGNWSVRTVLTCAVALGALTGTGAFPAASK 193
DB 190 QDNGGDADFVELYG----PSMRPLDFSWLSKLTLSSAL-VGACITLIGAYLGHK 239
RESULT 13
US-08-726-211-5
; Sequence 5, Application US/08726211
; Publication No. US20030012812A1
; GENERAL INFORMATION:
; APPLICANT: Tormo, Mar
; APPLICANT: Tari, Ana M.
; APPLICANT: Lopez-Berestein, Gabriel
; TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY
; TITLE OF INVENTION: LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
```

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STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726.211
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: UTXC:504
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-726-211-5

Query Match 40.8%; Score 410.5; DB 8; Length 239;
Best Local Similarity 37.0%; Pred. No. 1.1e-36;
Matches 87; Conservative 35; Mismatches 58; Indels 55; Gaps 5;

QY 9 DTRALVADFVGYKLRQKGYVCGAG-----PGE----- 35
DB 10 DNREIVMKYIHYKLSQRGYEWADGVGAAPGAPGIFSSQPGHTPHPAASRDPVART 69
QY 36 -----GPAADP-----LHOAMRAAGDEFETRRRTFSDLAACLHVTPGSAOQR 78
DB 70 SPLQTPAAPGAAGPALSPVPVPHLALRQAGDDFSRRYRGDFAEMSSQLHLTPPTARGR 129
QY 79 FTQVSDLEFGGPNMGRVLAFFVFGAALCAESVNKEMEPLVGVQVQVEMVAYLETRLADWI 138
DB 130 FATVVEELFRDGVNMGRIVAFEFEGGVMCVESVNREMSPLVDNIALMWMTEYLNRHLHTWI 189
QY 139 HSSGGWAEFTALYGDGALBEARLRGNWASVRTVLTGAVALGALVTVGAFPAASK 193
DB 190 QDNGGWDADFVLYG-----PSMRPLDFSWLSKLTLLSLAL-VGACITLGAYLSHK 239

RESULT 15
US-10-053-645A-21
; Sequence 21, Application US/10053645A
; Publication No. US20030176376A1
; GENERAL INFORMATION:
; APPLICANT: Robert E. Klem
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
; TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
; TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
; FILE REFERENCE: 10412-022-999
; CURRENT APPLICATION NUMBER: US/10/053.645A
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,244
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-053-645A-21

Query Match 40.8%; Score 410.5; DB 12; Length 239;
Best Local Similarity 37.0%; Pred. No. 1.1e-36;
Matches 87; Conservative 35; Mismatches 58; Indels 55; Gaps 5;

QY 9 DTRALVADFVGYKLRQKGYVCGAG-----PGE----- 35
DB 10 DNREIVMKYIHYKLSQRGYEWADGVGAAPGAPGIFSSQPGHTPHPAASRDPVART 69
QY 36 -----GPAADP-----LHOAMRAAGDEFETRRRTFSDLAACLHVTPGSAOQR 78
DB 70 SPLQTPAAPGAAGPALSPVPVPHLALRQAGDDFSRRYRGDFAEMSSQLHLTPPTARGR 129
QY 79 FTQVSDLEFGGPNMGRVLAFFVFGAALCAESVNKEMEPLVGVQVQVEMVAYLETRLADWI 138
DB 130 FATVVEELFRDGVNMGRIVAFEFEGGVMCVESVNREMSPLVDNIALMWMTEYLNRHLHTWI 189
QY 139 HSSGGWAEFTALYGDGALBEARLRGNWASVRTVLTGAVALGALVTVGAFPAASK 193
DB 190 QDNGGWDADFVLYG-----PSMRPLDFSWLSKLTLLSLAL-VGACITLGAYLSHK 239

Search completed: October 24, 2003, 11:04:40
Job time : 47.5 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 24, 2003, 10:44:00 ; Search time 25 Seconds
(without alignments)
742.422 Million cell updates/sec

Title: US-09-925-674A-7

Perfect score: 1007

Sequence: 1 MATPASAPDTRALVADFGV.....LFGAVALGALVTVGAFPAASK 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 761*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	428.5	42.6	233	2 I49056	bcl-x long - mouse
2	428.5	42.6	233	2 B47537	apoptosis regulator
3	424.5	42.2	233	2 S51761	BCL-X protein - ra
4	423.5	42.1	233	2 A37332	transforming prote
5	414	41.1	232	2 S24390	transforming prote
6	412.5	41.0	239	1 TVHUB1	transforming prote
7	412	40.9	236	2 I67432	BCL-2 - rat (fragm
8	407	40.4	236	2 I53744	transforming prote
9	406	40.3	236	1 TVMSA1	gene bcl-2 protein
10	404.5	40.2	233	2 I67431	transforming prote
11	403	40.0	236	2 J47383	BCL-X-Long - rat
12	378	37.5	190	2 A47537	B-cell lymphoma 2
13	377.5	37.5	214	2 I49057	apoptosis regulato
14	375.5	37.3	227	2 JE0203	bcl-x transmembran
15	356	35.4	216	2 B37332	apoptosis regulato
16	349.5	34.7	199	1 TVMSB1	transforming prote
17	346	34.4	205	1 TVHUB1	transforming prote
18	277.5	27.6	154	2 I58194	gene bcl-2 protein
19	182	18.1	170	2 I49055	bcl-x short - mous
20	176	17.5	211	2 S58873	Bak protein - huma
21	174	17.3	176	2 I67435	gene bcl-x-short pr
22	173	17.2	211	2 S58875	cdn-2 protein - hu
23	157.5	15.6	192	2 J47538	bcl-2-associated p
24	153	15.2	192	2 A47538	bcl-2-associated p
25	150	14.9	261	2 H8578	protein ced-9 [imp
26	150	14.9	280	2 A53189	apoptosis suppress
27	149.5	14.8	133	2 I53295	bcl-2-associated p
28	146.5	14.5	179	2 J47555	Bax-delta protein:
29	146.5	14.5	218	2 B47538	bcl-2-associated p

33	143	14.2	177	2 S54778	NR-13 protein - qu
31	141	14.0	255	2 J47567	Mcl-1a protein - z
32	137.5	13.7	143	2 I38921	bcl-2-associated p
33	118	11.7	175	2 I39055	bcl-2 related - hu
34	112	11.1	350	2 A47476	BCL2 homolog MCL1
35	105	10.4	172	2 I49449	hemopoietic-specif
36	91.5	9.1	301	2 I36534	probable lipase/es
37	89	8.8	185	2 B83217	hypothetical prote
38	87	8.6	3433	1 GNWVKV	genome polyprotein
39	85	8.4	270	2 A12598	dihydrodipicolinat
40	85	8.4	279	2 B97381	dihydrodipicolinat
41	84.5	8.4	358	1 AULCQB	glutamate-aminola
42	83	8.2	417	2 I39939	DNA binding protei
43	82.5	8.2	1440	1 GNWVJF	genome polyprotein
44	82.5	8.2	3432	1 GNWVJE	genome polyprotein
45	81.5	8.1	354	2 S52040	Gln 1.1 protein -

ALIGNMENTS

RESULT 1

I49056
bcl-x long - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I49056; S52866
R:Pang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A:Reference number: I49055; MUID:95052604; PMID:7963517
A:Accession: I49056
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-233 <RES>
A:Cross-references: EMBL:U0101; NID:G506647; PIDN:AAA82173.1; PID:G506648
R:Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
submitted to the EMBL Data Library, November 1994
A:Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line thr
A:Reference number: S52866
A:Accession: S52866
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-233 <KAM>
A:Cross-references: EMBL:X83574; NID:G695622; PIDN:CAA58557.1; PID:G695623
C:Superfamily: bcl transforming protein

Query Match	42.6%	Score 428.5;	DB 2;	Length: 233;
Best Local Similarity	41.3%;	Pred. No. 2.8e-32;		
Matches 93;	Conservative 22;	Mismatches 57;	Indels 53;	Gaps 4;
Cy	11	RALVADFVGYKLRQKGY-----	V 28	
Db	6	RELVDVDFSLYKLSQKGYKWSQFS	SDVEENRTEAPEETEARETTPSAINGNPSMH:ADSPAV	65
Cy	29	CGAGGEGEPAAD-----	PLHQAMRAAGDEFFTRFRRTFSDLAALQHLVTPGSAQQPFT	80
Db	66	NGA-TGHSSSLDAREVIMAAVKQALREAGDEFFELRYRRAFSDLTSLQHLTPGTAYQSGFE	124	
Cy	81	OYSDLEFQGGNMGRLVAFPFVFGAALCAESVYNKEPELVGQVQEMWVAYLETRLDWIHS	140	
Db	125	OYVNELFRDGNMGRLVAFPFVFGALCVESVDKEMQVLVSRIASWMAATYLNHDLEPHWIOE	184	
Cy	141	SGGWAFFALYGDGALEEARLRE--GNWASVRTVLTGAVLALGAL	183	
Db	185	NGGNDTFVDLYGNNAAESRKQGERFNFRLPTGMTVAGVLLGSL	229	

RESULT 2

B47537
apoptosis regulator bcl-xL - human
N:Alternate names: bcl-2-related protein
N:Contains: apoptosis regulator bcl-xs


```
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C;Accession: B47537; C47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A;Title: bcl-2, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A;Reference number: A47537; MUID:93364977; PMID:8358789
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 <BOI>
A;Cross-references: GB:L20121; NID:G510900; PIDN:CAA80661.1; PID:G510901
A;Accession: C47537
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-69, 'G', 71-125, 189-233 <BO2>
A;Cross-references: GB:L20122; NID:G623236; PIDN:CAA80662.1; PID:G623237
C;Genetics:
A;Gene: BCL2L
A;Cross-references: GDB:228079
C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; apoptosis
F;1-233/Product: apoptosis regulator bcl-xL #status predicted <WAT>
F;1-125, 189-233/Product: apoptosis regulator bcl-xS #status predicted <MA2>
Query Match 42.6%; Score 428.5; DB 2; Length 233;
Best Local Similarity 40.6%; Pred. No. 2.8e-32;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;
QY 11 RALVADFVGVKLRQKGY-----PLHQAMRAAGDEFETFRRTFSDLAALQHLVTPGSAQQRFTQ 39
Db 6 RELVDFVLSYKLSQKGYSWQFSQSDVENRTEAPEETSEMETPSAINGNPSWHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFETFRRTFSDLAALQHLVTPGSAQQRFTQ 81
Db 66 NGATAHSSLLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGAYQSFEQ 125
QY 82 VSEDFQGGPNWGRVLAFFVFGAALCAESVKNEMEPVGVQVQWVAYLETRADWIHSS 141
Db 126 VNELFRDGVNMGRIVAFVFGGALCVESVKNEMEPVGVQVQWVAYLETRADWIHSS 185
QY 142 GWAETALYDGALEEARLRE--GNWASVRTVLTGAVALGAL 183
Db 186 GWDTFVELYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229
RESULT 3
S51761
BCL-X protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
C;Accession: S51761; S51762
R;Michaelidis, T.M.
submitted to the EMBL Data Library, November 1994
A;Reference number: S51761
A;Accession: S51761
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <MIC>
A;Cross-references: EMBL:X82537; NID:G607176; PIDN:CAA57886.1; PID:G607177
A;Experimental source: embryonic; brain
A;Accession: S51762
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125, 189-233 <MI2>
A;Cross-references: EMBL:X82537; NID:G607176; PIDN:CAA57887.1; PID:G607178
A;Experimental source: embryonic; brain
A;Note: smaller form due to splicing
C;Genetics:
A;Introns: 125/3
C;Superfamily: bcl transforming protein
Query Match 42.2%; Score 424.5; DB 2; Length 233;
Best Local Similarity 41.3%; Pred. No. 6.5e-32;
Matches 92; Conservative 22; Mismatches 56; Indels 53; Gaps 4;
QY 13 LVADFVGVKLRQKGY-----PLHQAMRAAGDEFETFRRTFSDLAALQHLVTPGSAQQRFTQV 30
Db 8 LVDFLSYKLSQKGYSWQFSQSDVENRTEAPEETSEMETPSAINGNPSWHLADSPAVNG 67
QY 31 AGPGEGPAAD-----PLHQAMRAAGDEFETFRRTFSDLAALQHLVTPGSAQQRFTQV 82
Db 68 A-TGSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPGTAVQSFEQV 126
QY 83 SDELFOGGPNWGRVLAFFVFGAALCAESVKNEMEPVGVQVQWVAYLETRADWIHSSG 142
Db 127 VNELFRDGVNMGRIVAFVFGGALCVESVKNEMEPVGVQVQWVAYLETRADWIHSSG 186
QY 143 GWAETALYDGALEEARLRE--GNWASVRTVLTGAVALGAL 183
Db 187 GWDTFVELYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229
RESULT 4
A37332
transforming protein (bcl-2-alpha) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Feb-1997
C;Accession: A37332; S35453
R;Sguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a var
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: A37332
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-233 <EGU>
A;Cross-references: EMBL:D11381
C;Genetics:
A;Introns: 189/3
C;Superfamily: bcl transforming protein
C;Keywords: mitochondrion; transforming protein; transmembrane protein;
Query Match 42.1%; Score 423.5; DB 2; Length 233;
Best Local Similarity 38.0%; Pred. No. 8.1e-32;
Matches 97; Conservative 32; Mismatches 64; Indels 49; Gaps 4;
QY 9 DTRALVADFVGVKLRQKGYCGAG-----PGEGPAADP----- 41
Db 10 DNREIVLKYIHYKLSQKGYDMAAGEDRPVPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 69
QY 42 -----LHQAMRAAGDEFETFRRTFSDLAALQHLVTPGSAQQRFTQUSD 84
Db 70 AASEVPPAEGLEPAPPGVHLALRQAGDBFSRRYQDRFQMSGQLHTPTTAHGRFVAVVE 129
QY 85 ELFOGGPNWGRVLAFFVFGAALCAESVKNEMEPVGVQVQWVAYLETRADWIHSSG 144
Db 130 ELFRDGVNMGRIVAFVFGGVMCVSVNREMSPLVDNIATMTTEYLNRHLNWDQNG 189
QY 145 ABFTALYDGALEEARLREGNWASVRTVLTGAVALGALTVGAFFASK 193
Db 190 DAFVELYGN----SMRPLDFSWISLKTLS-LVLVGACITLGAYLGK 233
RESULT 5
S24390
transforming protein (Bcl-2) homolog - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S24390
R;Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
Biochim. Biophys. Acta 1132, 109-113, 1992
A;Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologu
A;Reference number: S24390; MUID:92379084; PMID:1511008
A;Accession: S24390
A;Status: preliminary
```

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A:Molecule type: mRNA
A:Residues: 1-232 <CAZ>
A:Cross-references: EMBL:Z11961; NID:G62969; PIDN:CAA780:9.1; PID:G62970
A:Superfamily: bcl transforming protein
C:Keywords: mitochondrion; transmembrane protein

Query Match 41.1%; Score 414; DB 2; Length 232;
Best Local Similarity 37.7%; Pred. No. 6.1e-31;
Matches 86; Conservative 32; Mismatches 62; Indels 48; Gaps 4;

QY 9 DTRALVADFVGYKLRQKGYVCGAG-----PGSGPAADP----- 41
Db 10 DNRDIVLKYIHYKLSQRYDWAAGEDPPVPPAPAPAAAPAAVAAACAGASHHSPSPAR 69
QY 42 -----LHOAMRAAGDEFTFRFTFSDLAAQLHVTGSAOQRFTQVSD 85
Db 70 LLVRCPLRGCAAPGVHIALRQAGDEFSRRYQDFQMSQLHLTPTATGRFVAVVEE 129
QY 86 LFQGGPNWGRVAVFVFGAALCAESVNKMEPLVGVQVQEWVAYLETRLADWIHSSGNA 145
Db 130 LFRDGVNVRIVAFVFGVGVNCSVNREMSPLVDNIATWNTYLNRLHNLWIDNGGWC 189
QY 146 EFTALYGDGALEEARREGNWAASVRTVLTGAVALGALVTVGAFPAASK 193
Db 190 AFVELYGN-----SNRPLDFSMISLKLILS-LVLVGACITLGAYLGHK 232

RESULT 6
TVHUAL
transforming protein bcl-2, splice form alpha - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence revision 07-Jun-1996 #text_change 15-Oct-1999
C:Accession: G37332; A29409; S02452; A24428; A27622; B27622
R: Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues
A:Reference number: A37332; MUID:92375724; PMID:1508712
A:Accession: G37332
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-239 <EGU>
A:Note: this report is a correction
R: Tsujimoto, Y.; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene for the B-cell lymphoma
A:Reference number: A29409; MUID:86259760; PMID:3523487
A:Accession: A29409
A:Molecule type: mRNA
A:Residues: 1-95, 'A', 97-109, 'G', 111-236, 'S', 238-239 <TSU>
A:Cross-references: GB:M13994; NID:G179366; PIDN:AAA51813.1; PID:G179367
A:Note: this sequence has been corrected in reference A37332
R: Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer, S.J.
EMBO J. 7, 123-131, 1988
A:Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2 gene
A:Reference number: S02452; MUID:88196071; PMID:2834197
A:Accession: S02452
A:Molecule type: mRNA
A:Residues: 1-239 <SEI>
R: Cleary, M.L.; Smith, S.D.; Sklar, J.
Cell 47, 19-28, 1986
A:Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin heavy chain enhancer
A:Reference number: A24428; MUID:87002484; PMID:2875799
A:Accession: A24428
A:Molecule type: mRNA
A:Residues: 1-58, 'T', 60-116, 'R', 118-239 <CLE>
A:Cross-references: GB:M14745; NID:G179370; PIDN:AAA35591.1; PID:G179371
R: Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakhtshi, A.
Oncogene Res. 2, 263-275, 1988
A:Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma: a study of the bcl-2 gene
A:Reference number: A27622; MUID:86217344; PMID:3285301
A:Accession: A27622
A:Molecule type: mRNA
A:Residues: 1-58, 'T', 60-239 <HUA>
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A:Accession: B27622
A:Molecule type: DNA
A:Residues: 1-6, 'S', 8-58, 'T', 60-128, 'C', 130-239 <HUA2>
A:Note: the sequence was determined from the germline gene
C:Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation
C:Genetics:
A:Gene: GDB:BCL2
A:Cross-references: GDB:119031; OMIM:151430
A:Map position: 18q21.3-18q21.3
C:Function:
A:Description: blocks apoptosis in hematopoietic cells
A:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; pre-B-cell leukemia

Query Match 41.0%; Score 412.5; DB 1; Length 239;
Best Local Similarity 37.0%; Pred. No. 8.7e-31;
Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;

QY 9 DTRALVADFVGYKLRQKGYVCGAG-----PGE----- 35
Db 10 DNRDIVLKYIHYKLSQRYDWAAGEDPPVPPAPAPAAAPGIFSSQPGHTPEPAASRDPVART 69
QY 36 -----GPAADP-----LHOAMRAAGDEFTFRFTFSDLAAQLHVTGSAOQR 78
Db 70 SPLQTPAAPGAAGPALSPVPVHLTLRQAGDPSRRYRDFAEISSQLHLTPPTARGR 129
QY 79 FTQVSDLELFGQGNWGRVAVFVFGAALCAESVNKMEPLVGVQVQEWVAYLETRLADWI 138
Db 130 FATVVEELFRDGVNVRIVAFVFGVGVNCSVNREMSPLVDNIATWNTYLNRLHNLWIDNGGWC 189
QY 139 HSSGWAFTALYGDGALEEARREGNWAASVRTVLTGAVALGALVTVGAFPAASK 193
Db 190 QDNGWDADFVELYG-----PSNRPLDFSMISLKLILS-LVLVGACITLGAYLGHK 239

RESULT 7
I67432
BCL-2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I67432
R: Tilly, J.L.; Tilly, K.I.; Kerton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equi-constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A:Reference number: I53295; MUID:95129487; PMID:7828536
A:Accession: I67432
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-236 <RES>
A:Cross-references: EMBL:U34964; NID:G1004378; PIDN:AAA7687.1; PID:G1004379
C:Superfamily: bcl transforming protein

Query Match 40.9%; Score 412; DB 2; Length 236;
Best Local Similarity 36.2%; Pred. No. 9.6e-31;
Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

QY 9 DTRALVADFVGYKLRQKGY----- 27
Db 10 DNRDIVLKYIHYKLSQRYDWAAGEDPPVPPAPAPAAAPGIFSSQPGHTPEPAASRDPVART 69
QY 28 -----VCGAGGCGPAADPLHOAMRAAGDEFTFRFTFSDLAAQLHVTGSAOQR 81
Db 70 SPLRPLVANAGPALSPVPVHLTLRQAGDPSRRYRDFAEISSQLHLTPPTARGR 129
QY 82 VSDLELFGQGNWGRVAVFVFGAALCAESVNKMEPLVGVQVQEWVAYLETRLADWIHSS 141
Db 130 VVEELFRDGVNVRIVAFVFGVGVNCSVNREMSPLVDNIATWNTYLNRLHNLWIDNGGWC 189
QY 142 GWAASFTALYGDGALEEARREGNWAASVRTVLTGAVALGALVTVGAFPAASK 193
Db 190 GWDADFVELYG-----PSNRPLDFSMISLKLILS-LVLVGACITLGAYLGHK 236
```

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RESULT 8
153744
gene bcl-2 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C:Accession: I53744
R:Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
Gene 140, 291-292, 1994
A:Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.
A:Reference number: I53744; MUID:94193015; PMID:8144041
A:Accession: I53744
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-236 <RES>
A:Cross-references: GB:L14680; NID:G4C8946; PID:AAA53662.1; PID:G4C8947
C:Genetics:
A:Gene: bcl-2
C:Superfamily: bcl transforming protein

Query Match 40.4%; Score 407; DB 2; Length 236;
Best Local Similarity 35.8%; Pred. No. 2.8e-30;
Matches 83; Conservative 34; Mismatches 63; Indels 52; Gaps 3;

QY 9 DTRALVADFVGYKLRQKGY-----PG----- 34
D 10 DNREIVMKYIHYKLSQGYEWDAGDADAAPLGAAPTGCIFSFQPSNPMPAVHREMAART 69
QY 35 -----EGPAADP-----LHOAMRAAGDEFETRFRTPSDLAOLHVTGPSAQORFTQ 81
D 70 SPLRPLVANAGPALSPVPPVHLTLRRAGDDFSRRYRDRDFAEMSSQLHLTPFTARGRFAT 129
QY 82 VSDLEFQGGNWRGLVAVFFVFGAALCAESVNKEMEPVGVQVQEMVAYLETRLADWIHSS 141
D 130 VVEELFRDGVNWRGRIVAVFFFGVGMVSVNRENSPLVDNIALWMTEYLNRLHLHTWIQDN 189
QY 142 GGAWEFTALYDGALEEARLRREGNWSVRTVLTGAVALGALVTVCFAFFASK 193
D 190 GGWDAFVELYG----PSMRPLDFSLKLTLLS-LPMVGCITLGAYLGHK 236

RESULT 10
167431
BCL-X-Long - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I67431
R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: constitutive bcl-2 and bcl-xiong messenger ribonucleic acid levels.
A:Reference number: I53295; MUID:95129487; PMID:7828536
A:Accession: I67431
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-233 <RES>
A:Cross-references: EMBL:U34963; NID:G1004376; PID:AAA77686.1; PID:G1004377
C:Superfamily: bcl transforming protein

Query Match 40.2%; Score 404.5; DB 2; Length 233;
Best Local Similarity 39.6%; Pred. No. 4.7e-30;
Matches 89; Conservative 22; Mismatches 61; Indels 53; Gaps 4;

QY 11 RALVADFVGYKLRQKGY-----V 28
D 6 RELVDFLSYKLSQGYSMWSQFSDVENRTPEAPETPSPNPNPSWHLADSPAV 65
QY 29 CGAGPGEPAAD-----PLHOAMRAAGDEFETRFRTPSDLAOLHVTGPSAQORFT 80
D 66 NGA-TGHSSSLDAREVLPMMAVKQALREAGDEFELRYRRAFSDLTSQLHTPTGTVYQSFE 124
QY 81 QVSDLEFQGGNWRGLVAVFFVFGAALCAESVNKEMEPVGVQVQEMVAYLETRLADWIHSS 140
D 125 QVVELFRDGVNWRGRIVAVSSSFGALCVESVDKEMQVLVSRIASWMMATYLNHLSPWIOE 184
QY 141 SGGWAEFTALYDGALEEARLRREGNWSVRTVLTGAVALGAL 183
D 185 NGWMDTFVDLYGNNTAPESRKQGERFNRWFLTGMTVAGVVLGSL 229

RESULT 11
JC7383
B-cell lymphoma 2 protein - Chinese hamster
C:Species: Cricetulus griseus (Chinese hamster)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 08-Dec-2000
C:Accession: JC7383
R:Tomicic, M.T.; Christmann, M.; Kaina, B.
Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A:Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A:Reference number: JC7383
A:Contents: Ovary
A:Accession: JC7383
A:Molecule type: mRNA
A:Residues: 1-236 <TOM>
A:Cross-references: GB:AJ271720
C:Comment: This protein has anti-apoptotic function, and supports cell survival.
C:Genetics:

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A:Gene: bcl-2
C:Superfamily: bcl transforming protein
C:Keywords: B-cell lymphoma; ovary

Query Match 40.0%; Score 403; DB 2; Length 236;
Best Local Similarity 35.3%; Pred. No. 6.5e-30;
Matches 82; Conservative 34; Mismatches 64; Indels 52; Gaps 3;
QY 9 DTRALVADPVGYKLRQGY----- 27
Db 10 DNREIVMKYIHYKLSQRYGWDVGEVDAAPLGAAPTFCIESFQESNPTPAVHRDMAAR 69
QY 28 -----VCGAGPGGPAADPLHQYRAAGDEFETFRRTSDLAALHVTFGSAQQRFTQ 81
Db 70 SPLRPVATTGPTLSPVPPVPHLTLRAGDDEFRRYRDFAEWSSQLHLTPFTARGFEAT 129
QY 82 VSDLEFGGPNWGRVLAFFVFGAALCAESVKNKEPLVGQVQVEMVAYLETRLDADWHS 141
Db 130 VVELFPRDGVNMGRIVAFFPFGGVNVCESVNRNSPLVDNIALWMTLEYLNRHLHTWIQDN 189
QY 142 GGMWAEFTALYGDGALEARRLRGNWASVRTLTGAVALGALVTGVAFFASK 193
Db 190 GGMWAEFTALYGDGALEARRLRGNWASVRTLTGAVALGALVTGVAFFASK 193
QY 190 GGMWAEFTALYGDGALEARRLRGNWASVRTLTGAVALGALVTGVAFFASK 193
Db 190 GGMWAEFTALYGDGALEARRLRGNWASVRTLTGAVALGALVTGVAFFASK 193

RESULT 12

A47537
apoptosis regulator bcl-x - chicken
C:Species: Gallus gallus (chicken)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C:Accession: A47537
R:Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A:Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptosis
A:Reference number: A47537; MUID:93364977; PMID:8358789
A:Accession: A47537
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-190 <BOI>
A:Cross-references: GB:223110; GBL:20120; NID:9510898; PIDN:CAA80657.1; PID:9510899
C:Superfamily: bcl transforming protein

Query Match 37.5%; Score 378; DB 2; Length 190;
Best Local Similarity 43.8%; Pred. No. 1e-27;
Matches 81; Conservative 14; Mismatches 44; Indels 46; Gaps 3;
QY 11 RALVADPVGYKLRQGY-----VCGAGPGGP----- 37
Db 6 RELVIDFVSYKLSQRYGWDVGEVDAAPLGAAPTFCIESFQESNPTPAVHRDMAAR 65
QY 38 -----ADPLHQYRAAGDEFETFRRTSDLAALHVTFGSAQQRFTQVSDZ 85
Db 66 VHRSSLEVHEIVRASDVQALRDAGDEFELRYRAAFSDLTSQLHITPGTAYQSFQVNE 125
QY 86 LFGGPNWGRVLAFFVFGAALCAESVKNKEPLVGQVQVEMVAYLETRLDADWHS 145
Db 126 LFGGPNWGRVLAFFVFGAALCAESVKNKEPLVGQVQVEMVAYLETRLDADWHS 145
QY 146 EFTAL 150
Db 186 R-TAL 189

RESULT 13

149057
bcl-x transmembrane deleted - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I49057
R:Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A:Reference number: I49055; MUID:95052604; PMID:7963517

A:Accession: I49057
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-214 <RES>
A:Cross-references: EXBL:U10102; NID:9506649; PIDN:AAA82174.1; PID:9506650
C:Genetics:
A:Gene: bcl-x-long
C:Superfamily: bcl transforming protein

Query Match 37.5%; Score 377.5; DB 2; Length 214;
Best Local Similarity 42.8%; Pred. No. 1.3e-27;
Matches 80; Conservative 16; Mismatches 40; Indels 51; Gaps 3;
QY 11 RALVADPVGYKLRQGY-----V 28
Db 6 RELVIDFVSYKLSQRYGWDVGEVDAAPLGAAPTFCIESFQESNPTPAVHRDMAAR 65
QY 29 CGAGPGGPAAD-----PLHQYRAAGDEFETFRRTSDLAALHVTFGSAQQRFT 80
Db 66 NGA-TGHSSLDAREVIMAAVKQALREAGDEFELRYRAAFSDLTSQLHITPGTAYQSF 124
QY 81 QVSDLEFGGPNWGRVLAFFVFGAALCAESVKNKEPLVGQVQVEMVAYLETRLDADWHS 140
Db 125 QVNELFRDGVNMGRIVAFFPFGGVNVCESVNRNSPLVDNIALWMTLEYLNRHLHTWIQDN 189
QY 141 SGWAEFTALYGDGALEARRLRGNWASVRTLTGAVALGALVTGVAFFASK 193
Db 185 NGGMDTF 191

RESULT 14

CE0203
apoptosis regulator bcl-x isoform - human
N:Alternate names: h-bcl-xbeta
C:Species: Homo sapiens (man)
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 16-Jul-1999
C:Accession: JE0203
R:Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E.
Biochem. Biophys. Res. Commun. 248, 147-152, 1998
A:Title: Identification of a human cDNA encoding a novel bcl-x isoform.
A:Reference number: JE0203; MUID:98340865; PMID:9675101
A:Accession: JE0203
A:Molecule type: mRNA
A:Residues: 1-227 <BAN>
A:Cross-references: GB:U72398; NID:gl622940; PIDN:AAB17354.1; PID:gl622941
C:Genetics:
A:Gene: bcl-x
A:Map position: 20
C:Superfamily: bcl transforming protein

Query Match 37.3%; Score 375.5; DB 2; Length 227;
Best Local Similarity 40.8%; Pred. No. 2.2e-27;
Matches 82; Conservative 18; Mismatches 50; Indels 51; Gaps 3;
QY 11 RALVADPVGYKLRQGY-----V 28
Db 6 RELVIDFVSYKLSQRYGWDVGEVDAAPLGAAPTFCIESFQESNPTPAVHRDMAAR 65
QY 29 CGAGPGGPAAD-----PLHQYRAAGDEFETFRRTSDLAALHVTFGSAQQRFT 80
Db 66 NGA-TGHSSLDAREVIMAAVKQALREAGDEFELRYRAAFSDLTSQLHITPGTAYQSF 124
QY 81 QVSDLEFGGPNWGRVLAFFVFGAALCAESVKNKEPLVGQVQVEMVAYLETRLDADWHS 140
Db 125 QVNELFRDGVNMGRIVAFFPFGGVNVCESVNRNSPLVDNIALWMTLEYLNRHLHTWIQDN 189
QY 141 SGWAEFTALYGDGALEARRLRGNWASVRTLTGAVALGALVTGVAFFASK 193
Db 185 NGGMDTF 191

RESULT 15

B37332

Search completed: October 24, 2003, 10:52:02
Job time : 27 secs

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OM protein - protein search, using sw model

Run on: October 24, 2003, 10:26:35 ; Search time 13.5 Seconds
(without alignments)
672.308 Million cell updates/sec

Title: US-09-925-674A-7

Perfect score: 1007

Sequence: 1 MATPASAPDTRALVADPVGY.....LTCAVALGALVTVGAFASK 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1007	100.0	193	1 BCLW_HUMAN	Q92843 homo sapien
2	1000	99.3	193	1 BCLW_HUMAN	P70345 mus musculus
3	646.5	64.2	228	1 ARI_XENLA	Q37827 xenopus lae
4	432.5	42.9	229	1 BCLX_CHICK	Q7816 gallus gall
5	431.5	42.9	233	1 BCLX_PIG	C77737 sus scrofa
6	428.5	42.6	233	1 BCLX_HUMAN	Q7817 homo sapien
7	428.5	42.6	233	1 BCLX_MOUSE	Q64373 mus musculus
8	428.5	42.6	233	1 BCLX_RAT	P53563 rattus norv
9	423.5	42.1	233	1 BCL2_CHICK	Q30709 gallus gall
10	416.5	41.4	229	1 BCL2_BOVIN	O32718 bos taurus
11	414	41.1	236	1 BCL2_RAT	P49950 rattus norv
12	413	41.0	236	1 BCL2_MOUSE	P10417 mus musculus
13	412.5	41.0	239	1 BCL2_HUMAN	P10415 homo sapien
14	403	40.0	236	1 BCL2_CRILLO	Q93378 cricetus
15	371	36.8	204	1 ARI1_XENLA	Q31828 xenopus lae
16	177.5	17.6	208	1 BAK_MOUSE	O38734 mus musculus
17	176	17.5	211	1 BAK_HUMAN	Q3611 homo sapien
18	173	17.2	211	1 BAX2_HUMAN	Q13014 homo sapien
19	155.5	15.4	192	1 BAXA_MOUSE	Q07813 mus musculus
20	154.5	15.3	192	1 BAXA_RAT	Q63690 rattus norv
21	153	15.2	192	1 BAXA_HUMAN	Q07812 homo sapien
22	150	14.9	280	1 CEE9_CAEEL	P41958 caenorhabdi
23	147	14.6	192	1 BAXA_BOVIN	O27703 bos taurus
24	146.5	14.5	218	1 BAXA_HUMAN	Q07814 homo sapien
25	143	14.2	177	1 NR13_COTJA	Q90343 coturnix co
26	137.5	13.7	143	1 BAXD_HUMAN	P55269 homo sapien
27	136.5	13.6	271	1 CED9_CAEER	P41957 caenorhabdi
28	118	11.7	175	1 BFL1_HUMAN	Q16548 homo sapien
29	117	11.6	194	1 BCLB_HUMAN	Q9h36 homo sapien
30	112	11.1	350	1 MCL1_HUMAN	Q7820 homo sapien
31	105	10.4	172	1 BFL1_MOUSE	Q07440 mus musculus
32	99.5	9.9	179	1 EAR_ASPM2	Q07819 african swi
33	98.5	9.8	179	1 EAR_ASFE7	P42485 african swi

RESULT 1

BCLW_HUMAN

ID BCLW_HUMAN STANDARD; PRT; 193 AA.
AC Q92843;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Apoptosis regulator Bcl-w (Bcl2-like 2 protein).
GN BCL2L2 OR BCLW OR KIAA0271.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358615; PubMed=8761287;
RA Gibson L., Holmgren S.P., Huang D.C., Bernard C., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival."
RL Oncogene 13:665-675(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97191544; PubMed=9039502;
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.,
RT Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RL analysis of cDNA clones from cell line KG-1 and brain."
RNA Res. 3:321-329(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madar A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
CC -!- FUNCTION: PROMOTES CELL SURVIVAL.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

34 98.5 9.8 179 1 EAR_ASFE4
35 87 8.6 3433 1 POLG_KUNJM
36 85.5 8.5 358 1 GLNA_LACSA
37 85 8.4 275 1 DAPB_AGRTS
38 83.5 8.3 660 1 SOHC_BRAJA
39 82.5 8.2 1440 1 POLG_JAEVN
40 82.5 8.2 3432 1 POLG_JAEVN
41 90 7.9 541 1 PTCD_MOUSE
42 79.5 7.9 872 1 SYA_STRPN
43 79 7.8 396 1 PORB_PYRTU
44 79 7.8 541 1 PTCD_RAT
45 79 7.8 3430 1 POLG_WNV

ALIGNMENTS


```
DB 61 FSLAAQJHYTPGSAQQRFTQVSDLEFGGPNWGRULVAFVFGAALCAESVKNKEMPELVG 120
QY 121 QVQEMVAYLETRIAWHSSGGWAEFTALYGDGALEEARLRREGNWSVRVLTGVAL 160
DB 121 QVQDMVAYLETRIAWHSSGGWAEFTALYGDGALEEARLRREGNWSVRVLTGVAL 180
QY 161 GALVTGCAFFASK 193
DB 181 GALVTGCAFFASK 193

RESULT 3
ID ARI XENLA STANDARD; PRT; 228 AA.
AC Q91827;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptosis regulator R1 (XRI) (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=953311613; PubMed=7607538;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
cell-survival genes.";
RL Gene 158:171-179(1995).
CC -!- FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.
CC -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -!- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
BRAIN OF MID-METAMORPHIC TO POST-METAMORPHIC TADPOLES AND
ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC -----
DR EMBL; X82462; CAA57845.1; ..
DR HSSP; Q07817; 1MAZ.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM03337; BCL2; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane.
FT NON_TER 1 1
FT DOMAIN 120 139 BH1.
FT DOMAIN 171 186 BH2.
FT TRANSMEM 207 227 POTENTIAL.
SQ SEQUENCE 228 AA; 25068 MW; C499D449A585F8A9 CRC64;

Query Match 64.2%; Score 646.5; DB 1; Length 228;
Best Local Similarity 67.9%; Pred. No. 5e-51;
Matches 125; Conservative 21; Mismatches 35; Indels 3; Gaps 1;
QY 10 TRALVADVGYKLRQGVCGAGPGGPAADPJDQAMRAAGDETFRRRTFSDLAALQH 69
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DB 48 SRALVEDLVRYKLCQSRSLV---PEPSGAASCALHSAMRAAGDEFEERFQAFSEISTQIH 104
QY 70 VTPGSAQORFTQVSDLEFGGPNWGRULVAFVFGAALCAESVKNKEMPELVGQVQEMVAY 159
DB 105 VTPGTARFAEVAAGSLFQGVWNGRIVAFVFGAALCAESVKNKEMSPLLPRICDWMVTY 164
QY 130 LETRLADMIRHSSGGWAEFTALYGDGALEEARLRREGNWSVRVLTGVALGALVTVGAF 199
DB 165 LETNLRDWIQSNGWNGFLTYLGDGALEEARLRREGNWSLTKLTGVALGALMTVGAL 224
QY 190 FASK 193
DB 225 FASK 228

RESULT 4
BCX CHICK STANDARD; PRT; 229 AA.
ID BCLX_CHICK
AC Q07816; Q98908;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-X (BCL2-like 1 protein).
GN BCL2L1 OR BCLX OR BCL-X.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=93364977; PubMed=8358789;
RA Boise L.H., Gonzales-Garcia M., Postema C.E., Ding L., Lindsten T.,
Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
of apoptotic cell death.";
RL Cell 74:597-608(1993);
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=Hubbard White Mountain; TISSUE=Testis;
RX MEDLINE=97264485; PubMed=9110311;
RA Vilagrasa X., Mezquita C., Mezquita J.;
RT "Differential expression of bcl-2 and bcl-x during chicken
spermatogenesis.";
RL Mol. Reprod. Dev. 47:26-29(1997).
CC -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
ENVELOPE (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=Long;
isoId=Q07816-1; Sequence=Displayed;
Name=Short;
isoId=Q07816-2; Sequence=VSP_000514;
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
DEVELOPMENT.
CC -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
APOPTOTIC ACTIVITY (BY SIMILARITY).
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC EMBL; Z23110; CAAB0657.1; -;
CC EMBL; U26645; AAB07677.1; -;
DR PIR; A47537; A47537.
DR HSSP; P53563; IAF3.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; Bcl-2; 1.
DR PROSITE; PS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01258; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS0063; BH4_2; 1.
DR Apoptosis; Transmembrane; Alternative splicing.
FT DOMAIN 4 24 BH4.
FT DOMAIN 82 96 BH3.
FT DOMAIN 125 144 BH1.
FT DOMAIN 176 191 BH2.
FT TRANSMEM 206 223 POTENTIAL.
FT VARSPLIC 185 229 ERFVLYGNNAALRKQETFNKMLTGATVAGVLLGSJ
FT LSRK -> VITALP (in isoform Short).
FT /FTid=VSP C00514.
SQ SEQUENCE 229 AA; 25733 MW; A57D3A4D04C0E9DA CRC64;

Query Match 42.9%; Score 432.5; DB 1; Length 229;
Best Local Similarity 41.7%; Pred. No. 8.3e-32;
Matches 95; Conservative 22; Mismatches 62; Indels 49; Gaps 4;
QY 11 RALVADFVGYKLRQKY-----VCGAGCGEGP----- 37
Db 6 RELVIDFVYKLSRGHCWSELEEDENRDTAAEAMDSVKNSPSWHPAGHVNGAT 65
QY 38 -----AADPLHQAMRAAGDEFETRFRRTFSDLAALQHLVTPGSAQORFTQVSD 85
Db 66 VHRSSLEVHEIVRASDVQALRDAGDEFELRYRRAFSDLTSQLHTPTGTAYQFEQVNE 125
QY 86 LFQGGPNWGLVAFVFGAALCAESVKNKEPLVGVQVEMWVAYLETRLDADWTHSSGWA 145
Db 126 LFHDGVNMGRIVAFVFGGALCVESVDKEMRVLVGRIVSNMTYLTDLHDPWIOENGWNE 185
QY 146 EFTALYGDGALAEARRLRGNWASVRTLTGAVAGALVTVGAFFASK 193
Db 186 RFVDLYGNNA---AALRKQETFNKMLTGATVAGVLL-LGSLLSRK 229

RESULT 5
BCLX_PIG STANDARD; PRT; 233 AA.
AC 07737;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Apoptosis regulator Bcl-X (BCL2-like 1 protein).
GN BCL2L1 OR BCL2L OR BCLX.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A. PubMed=10072723;
RA Batting B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT "Quantification of cardioprotective gene expression in porcine
RT short-term hibernating myocardium.";

RJ J. Mol. Cell. Cardiol. 31:147-158(1999).
CC -!- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-x(2) anti-
CC apoptotic activity is inhibited by association with SIVA isoform
CC 1. Inhibits activation of caspases (By similarity). Appears to
CC regulate cell death by blocking the voltage-dependent anion
CC channel (VDAC) by binding to it and preventing the release of the
CC caspase activator, cytochrome c, from the mitochondrial membrane.
CC -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC similarity). Heterodimerization with BAX does not seem to be
CC required for anti-apoptotic activity (By similarity). Isoform Bcl-
CC x(L) binds to Siva isoform 1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC envelope (By similarity).
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis (By
CC similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC apoptotic activity (By similarity).
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC or send an email to license@isb-sib.ch).

CC EMBL; AJ001203; CAAB04597.1; -;
DR HSSP; Q07817; IMAZ.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; Bcl-2; 1.
DR PROSITE; PS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01258; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS0063; BH4_2; 1.
KW Apoptosis; Mitochondrion; Transmembrane.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226 POTENTIAL.
SQ SEQUENCE 233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;

Query Match 42.9%; Score 431.5; DB 1; Length 233;
Best Local Similarity 41.8%; Pred. No. 1e-31;
Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;
QY 11 RALVADFVGYKLRQKY-----V 28
Db 6 RELVDFLSYKLSQKYSQSWQTFDVEENRTEAPECTSEAEETPSAINGNPSMHLADSPAV 65
QY 29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAALQHLVTPGSAQORFT 80
Db 66 NGA-TGHSSLDAREVPMVAVKQALREAGDEFELRYRRAFSDLTSQLHTPTGTAYQSGFE 124
QY 81 QVSDLEFQGGPNWGLVAFVFGAALCAESVKNKEPLVGVQVEMWVAYLETRLDADWTHS 140
Db 125 QVNLNLFDRGVNMGRIVAFVFGGALCVESVDKEMRVLVSRVATWMA-TYLNLDHLEPWICE 184

Oy 141 SGGWAETALYDGCALBEARLRRE - GNMASVRTLTGVALGAL 183
 BCLX HUMAN STANDARD; PRT: 233 AA.
 AC 007817; Q92976;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DE 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Apoptosis regulator Bcl-x (BCL2-like 1 protein).
 GN BCL2L1 OR BCL2L OR BCLX.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
 RX MEDLINE=93364977; PubMed=8358789;
 RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
 RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
 RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
 RT of apoptotic cell death.";
 RL Cell 74:597-608(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM X (BETA)).
 RA Inohara N., Ohta S.;
 RL Submitted (OCT-1996) to the ENBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM X(L)).
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Aleuchuk S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huly S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.
 RX MEDLINE=95372373; PubMed=7644501;
 RA Sedlak T.W., Oltvai Z.N., Yang E., Wang K., Boise J.H., Thompson C.B.,
 RA Korsmeyer S.J.;
 RA "Multiple Bcl-2 family members demonstrate selective dimerizations
 RT with Bax.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).
 RN [5]
 RP MUTAGENESIS OF BH1 AND BH2 DOMAINS.
 RX MEDLINE=96170038; PubMed=8596636;
 RA Cheng E.H.-Y., Levine B., Boise J.H., Thompson C.B., Hardwick J.X.,
 RA Korsmeyer S.J.;
 RT "Bax-independent inhibition of apoptosis by Bcl-XL.";
 RL Nature 379:554-556(1996).
 RN [6]
 RP INTERACTION WITH SIVA.
 RX PubMed=12011449;
 RA

RA Xue L., Chu F., Cheng Y., Sun X., Borthakur A., Ramarao M., Pandey P.,
 RA Wu M., Schlossman S.F., Prasad K.V.S.;
 RT "Siva-1 binds to and inhibits BCL-X(L)-mediated protection against UV
 RT radiation-induced apoptosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:6925-6930(2002).
 RN [7]
 RP STRUCTURE BY NMR OF 1-209.
 RX MEDLINE=97172562; PubMed=9020082;
 RA Sattler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E.,
 RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
 RA Thompson C.B., Pesik S.W.;
 RT "Structure of Bcl-xL-Bak peptide complex: recognition between
 RT regulators of apoptosis.";
 RL Science 275:983-986(1997).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY [2.2 ANGSTROMS], AND STRUCTURE BY NMR OF 1-209.
 RX MEDLINE=96256675; PubMed=8692274;
 RA Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
 RA Yoon H.S., Nettlesheim D., Chang B.S., Thompson C.B., Wong S.L.,
 RA Ng S.L., Pesik S.W.;
 RT "X-ray and NMR structure of human Bcl-xL, an inhibitor of programmed
 RT cell death.";
 RL Nature 381:335-341(1996).
 RN [9]
 RP CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.
 RX MEDLINE=98118550; PubMed=9435230;
 RA Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,
 RA Takahashi A., Kastan M.B., Griffin D.E., Earnshaw M.A.,
 RA Hardwick J.M.;
 RT "Modulation of cell death by Bcl-xL through caspase interaction.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).
 CC -!- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-x(L) anti-
 CC apoptotic activity is inhibited by association with SIVA isoform
 CC 1. Inhibits activation of caspases (By similarity). Appears to
 CC regulate cell death by blocking the voltage-dependent anion
 CC channel (VDAC) by binding to it and preventing the release of the
 CC caspase activator, cytochrome c, from the mitochondrial membrane.
 CC The Bcl-x(S) isoform promotes apoptosis.
 CC -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2.
 CC Heterodimerization with BAX does not seem to be required for anti-
 CC apoptotic activity. Isoform Bcl-x(L) binds to Siva isoform 1.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
 CC envelope (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=Bcl-X(L);
 CC IsoId=Q07817-1; Sequence=Displayed;
 CC Name=Bcl-X(S);
 CC IsoId=Q07817-2; Sequence=VSP_000515;
 CC Name=Bcl-X(beta);
 CC IsoId=Q07817-3; Sequence=VSP_000516;
 CC -!- TISSUE SPECIFICITY: Bcl-x(S) is expressed at high levels in cells
 CC that undergo a high rate of turnover, such as developing
 CC lymphocytes. In contrast, Bcl-x(L) is found in tissues containing
 CC long-lived postmitotic cells, such as adult brain.
 CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
 CC The BH1 and BH2 domains are required for both heterodimerization
 CC with other Bcl2 family members and for repression of cell death.
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
 CC activity.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
Endocrinology 136:232-241(1995).

[5]

X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

MEDLINE=98010630; PubMed=934936;

Aritomi M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,

Morikawa K.;

"Crystal structure of rat Bcl-xL. Implications for the function of

the Bcl-2 protein family.";

J. Biol. Chem. 272:27886-27892(1997).

CC -!- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-x(L) anti-

apoptotic activity is inhibited by association with SIVA isoform

1. Inhibits activation of caspases (By similarity). Appears to

regulate cell death by blocking the voltage-dependent anion

channel (VDAC) by binding to it and preventing the release of the

caspase activator, cytochrome c, from the mitochondrial membrane.

The Bcl-x(S) and Bcl-x(beta) isoforms promote apoptosis.

CC -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By

similarity). Heterodimerization with BAX does not seem to be

required for anti-apoptotic activity (By similarity). Isoform Bcl-

x(L) binds to Siva isoform 1 (By similarity).

CC -!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear

envelope (By similarity).

CC -!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=3;

Name=Bcl-X(L);

isoId=P53563-1; Sequence=Displayed;

Name=Bcl-X(S);

isoId=P53563-2; Sequence=VSP_000520;

Name=Bcl-X(beta);

isoId=P53563-3; Sequence=VSP_000521;

CC -!- TISSUE SPECIFICITY: Expressed in most tissues. Bcl-x(beta) is

specifically expressed in cerebellum, heart, and thymus. In the

ovary, the predominant form is Bcl-x(L), with a small but

detectable level of Bcl-x(S).

CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.

The BH1 and BH2 domains are required for both heterodimerization

with other Bcl2 family members and for repression of cell death.

CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The

cleaved protein, lacking the BH4 domain, has pro-apoptotic

activity (By similarity).

CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

or send an email to license@isb-sib.ch).

DR EMBL: X82537; CRA57886.1; -

DR EMBL: X82537; CRA57887.1; -

DR EMBL: U10579; AAB19257.1; -

DR EMBL: U72350; AAB17353.1; -

DR EMBL: U72349; AAB17352.1; -

DR EMBL: U34963; AAA77686.1; -

DR EMBL: S76513; AAC60701.1; ALT_INIT.

DR EMBL: S78284; AAC60702.1; -

DR PIR: I67431; I67431.

DR PIR: S51761; S51761.

DR PDB: 1AF3; 07-JUL-97.

DR InterPro: IPR000712; Bcl2 BH.

DR InterPro: IPR003093; Bcl2-BH4.

DR InterPro: IPR002475; Bcl2_family.

DR InterPro: IPR004725; Bcl2_reg.

DR Pfam: PF00452; Bcl-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART: SM00337; BCL; 1.

DR SMART: SM00265; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PS00062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS00063; BH4_2; 1.
KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
3D-structure.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226 POTENTIAL.
FT VARSPPLIC 126 188 Missing (in isoform Bcl-X(S)).
FT VARSPPLIC 189 233 /FTID=VSP_000520
DTFVDLYGNNAASRSKQERFNRWF.TGMTVAGVVLGSL
IDYGDIPGLL (in isoform Bcl-X(beta)).
FSRK -> VRTPLVCPPLVCLSSVEIPNCFWSPGMVVED
/FTID=VSP_000521.
R -> Q (IN REF. 1).
F -> S (IN REF. 2).
A -> E (IN REF. 2).
I -> L (IN REF. 4).
A -> V (IN REF. 4).
FF -> SS (IN REF. 4).
A -> T (IN REF. 4).
A -> P (IN REF. 4).

CONFLICT 6 6
CONFLICT 12 12
CONFLICT 64 64
CONFLICT 81 81
CONFLICT 119 119
CONFLICT 143 144
CONFLICT 199 199
CONFLICT 201 201
HELIX 4 19
TURN 20 21
TURN 25 28
TURN 82 83
HELIX 84 100
HELIX 106 112
TURN 116 117
HELIX 120 127
TURN 132 133
HELIX 137 156
TURN 157 158
TURN 160 161
HELIX 162 177
TURN 178 178
HELIX 179 184
TURN 185 186
HELIX 187 195
SEQUENCE 233 AA; 26158 MW; 2B62B6C63864BC8F CRC64;

Query Match 42.6%; Score 428.5; DB 1; Length 233;

Best Local Similarity 41.3%; Pred. No. 1.9e-31;

Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADFVGYKLRQKGY-----V 28
DB 6 RELVDFLSYKLSQGYSWQSQFVEENRTEPTEPETPSAINGNP2SHLADSPAV 65
QY 29 CGAGGEGPAAD-----PLHQAMRAAGDEPTEFRFRFTSDLAQLHVTGSAQRF 80
DB 66 NGA-TGHSSSLDAREVIMAAVKQALREAGDEFFELRYRRAFSDLTSLHITPGTAYQSFE 124
QY 81 QVSDLEFGGNNWGLVAFVFGAALCAESVYKMEPLVGOVQEMWVAYLETRLDWTHS 140
DB 125 QVNNELFRDGVNNGRIVAFVFGGALCVESVDKMQVLVSRIASWMTYLNHLEPWICE 184
QY 141 SGWAEFTALYGDGALBEARLRE--GNWASVRTVLTCALVALGAL 183
DB 185 NGGWTFTVDLYGNNAASRSKQERFNRWF.LTGMTVAGVVLGSL 229

RESULT 9
BCL2_CHECK
ID BCL2_CHECK STANDARD; PRT; 233 AA.

domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
 SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum (By similarity).
 DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).
 PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphatase 2A (P22A) (By similarity).
 PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).
 SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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EMBL: U92434; AAB53319.1; -
 HSSP: Q07817; IMAZ.
 InterPro: IPR000712; Bcl2_BH.
 InterPro: IPR003093; Bcl2_BH4.
 InterPro: IPR002475; Bcl2_family.
 InterPro: IPR004725; Bcl2_reg.
 Pfam: PF00452; Bcl-2; 1.
 Pfam: PF02180; BH4; 1.
 SMART: SM00337; BCL; 1.
 SMART: SM00265; BH4; 1.
 TIGRFAMs: TIGR00865; bcl-2; 1.
 PROSITE: P550062; BCL2_FAMILY; 1.
 PROSITE: P501080; BH1; 1.
 PROSITE: P501258; BH2; 1.
 PROSITE: P501259; BH3; 1.
 PROSITE: P501260; BH4; 1.
 PROSITE: P50063; BH4_2; 1.
 Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
 DOMAIN 10 30 BH4.
 DOMAIN 64 68 POLY-PRO.
 DOMAIN 69 72 POLY-ALA.
 DOMAIN 83 97 BH3.
 DOMAIN 126 145 BH1.
 DOMAIN 177 192 BH2.
 TRANSMEM 202 223 POTENTIAL.
 SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
 MOD_RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
 SEQUENCE 229 AA; 25099 MW; AD1DD0AF98FF1D CRC64;

Query Match 41.4%; Score 416.5; DB 1; Length 229;
 Best Local Similarity 38.2%; Pred. No. 2,3e-30;
 Matches 86; Conservative 35; Mismatches 59; Indels 45; Gaps 5;
 9 DTRALVADPVGKLRQKGVCGAG-----PGE----- 35
 10 DNREIVMKYHKLSQGVEMDAGAPGAPGAPGILSSQGRTPAFRTSPPPPPA 69
 36 ---GPAADP-----LQAMPAAGDETFRTFTSLAQLHVTGSAQORFTQVSDLEFQ 88
 70 AAGPAPSPVPVPHVLTURQAGDDFSRRYRKRDFAEISSQLHETPTTAKERFATVVEELFR 129

QY 89 GGNWGRVAFVFEFGALCAESVKNEMEPVLGVQVQEMWVAYLETRLADWIHSSGWAFT 148
 DB 130 GJVNWGRVAFVFEFGVNCVSVREMSPLVDSIALNWTETLNRHLHTWIOGNGWDAFV 189
 QY 149 ALYDGALEAZARRLRREGNWSVRTVLTGAVALGALVTGVGAFFASK 193
 DB 190 ELYG----PSMRPLDFDSWLSLKALLSLAL-VGACITLGAIVLGHK 229
 RESULT 11
 BCL2 RAT
 ID BCL2 RAT STANDARD; PRT; 236 AA.
 AC P49950; Q62837; Q64032;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2 OR BCL-2.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94193015; PubMed=8744041;
 RA Sato T., Irie S., Krajewski S., Reed J.C.;
 RT "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
 RL Gene 140:291-292(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
 RX MEDLINE=95129487; PubMed=7828536;
 RA Tilly J.L., Tilly K.I., Kenton M.L., Conson A.L.;
 RT "Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-x long messenger ribonucleic acid levels.";
 RL Endocrinology 136:232-241(1995).
 RN [3]
 RP SEQUENCE OF 19-172 FROM N.A.
 RX MEDLINE=95059917; PubMed=7969891;
 RA Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H., Lindholm D.;
 RT "bcl-2 messenger RNA is localized in neurons of the developing and adult rat brain.";
 RL Neuroscience 61:165-177(1994).
 CC -! FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphomatopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1).
 CC -! SUBUNIT: Forms homodimers, and heterodimers with BAX, BAK and Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
 CC -! SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -! TISSUE SPECIFICITY: Expressed in a variety of tissues, with highest levels in reproductive tissues. In the adult brain, expression is localized in mitral cells of the olfactory bulb, granule and pyramidal neurons of hippocampus, pontine nuclei, cerebellar granule neurons, and in ependymal cells. In prenatal brain, expression is higher and localized in the neuroepithelium and in the cortical plate.
 CC -! DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).
 CC -! PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and

130 VVEELFDGYNWGRIVAFEFQGWCMVSNRPMSPVDNIALMWTYLNRLHTWICDN 189
142 GGWAEFTALYDGCALGAEARRLREGNWSVRTVLTGAVAGLGAJVTVGAFASK 193
190 GGGWDAFVELYGV---FSMRPLDFDWSLWLSKTLTSLAL-VGACITLGA/YGHK 236

RESULT 13
BCL2 HUMAN
ID BCL2 HUMAN STANDARD; PRT: 239 AA.
P10415; P10416; Q13842; Q16197;
C1-MAR-1989 (Rel. 10, Created)
C1-APR-1993 (Rel. 25, Last sequence update)
I5-SEP-2003 (Rel. 42, Last annotation update)
DE Apoptosis regulator Bcl-2.
BCL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RX MEDLINE=86259760; PubMed=3523487;
RA "Tsujimoto Y., Croce C.M.;
RT "Analysis of the structure, transcripts, and protein products of
RT bcl-2, the gene involved in human follicular lymphoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN [2]
RP REVISIONS TO 96; I10 AND 237.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RT in a variety of tissues including lymphoid and neuronal organs in
RT adult and embryo.";
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=87002486; PubMed=2875799;
RA Cleary M.L., Smith S.D., Sklar J.;
RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-
RT 2/immunoglobulin transcript resulting from the t(14;18)
RT translocation.";
RL Cell 47:19-28(1986).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=88196071; PubMed=2834197;
RA Seto M., Jaeger M., Hockett R.D., Graninger W., Bennett S.,
RA Goldman P., Korsmeyer S.J.;
RT "Alternative promoters and exons, somatic mutation and deregulation
RT of the Bcl-2-19 fusion gene in lymphoma.";
RL EMBC J. 7:123-131(1988).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX T-SSUE-Testis;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Sculer G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rickard S.A., McEwan P.J., McKernan K.J., Malek J.A., Guraratne P.H.,
RA Boschak S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;


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QY 36 -----GPAADP-----LH0AVRAAGDEFTFRFTFSDLAAQLHVTGSAQQR 78
D 70 SPLQTPAAGAAAGPALSPVPPVHLTLRQAGDDFSRRYRSDFAEMSSQLHLPF--ARGR 129
QY 79 FTQVSDDELFOGPNWGRVLAFFVFGAALCAESVKNEMEPVGVQVQVWVAYLETRADWI 138
D 130 FATVEELFRDGVNMGRIVAFFEGGVNMCVSNREMSPLVDNIALMNTYLNRLHHTWI 189
QY 139 HSSGGAETALYDGALEARRREGNWSVRTVLTGAVALGALVTGGAFFASK 193
D 190 QDNGWDAFVELYG-----PSNRPLDFSWLSLKLTLSSAL-VGACITLGLAYLGHK 239

RESULT 14
ID BCL2 CRILO STANDARD; PRT; 236 AA.
AC Q9JUV8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Sukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetidae;
OC Cricetus.
ON NCBI_TaxID=10030;
RX TISSUE=Ovary;
RC SEQUENCE FROM N.A.
RX MEDLINE=20431763; PubMed=10973819;
RA Tomacic M.T., Christmann M., Kaina B.;
RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
RL protein."
RL Biochem. Biophys. Res. Commun. 275:899-903(2000).
RN [2]
RP SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES.
RX MEDLINE=21092839; PubMed=1118062;
RA Tomacic M.T., Kaina B.;
RT "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
RL and caspase-3."
RL Biochem. Biophys. Res. Commun. 281:404-408(2001).
CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphomatopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1) (By similarity).
CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BHI and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAF-1 (By similarity).
CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle (By similarity). In
CC the absence of growth factors, Bcl2 appears to be phosphorylated
CC by other protein kinases such as ERKs and stress-activated kinases
CC (By similarity). Dephosphorylation by protein phosphatase 2A (PP2A)
CC (By similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

```

```

CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC -----
CC EMBL; AJ271720; CAB92245.1; --
CC FIR; JC7383; JC7383.
CC HSP; Q07817; IMAZ.
CC InterPro; IPR000712; Bcl2_BH.
CC InterPro; IPR003093; Bcl2_BH4.
CC InterPro; IPR002475; Bcl2_family.
CC InterPro; IPR004725; Bcl2_reg.
CC Pfam; PF00452; Bcl-2; 1.
CC Pfam; PF02180; BH4; 1.
CC SMART; SM00337; BCL; 1.
CC SMART; SM00265; BH4; 1.
CC TIGRFAMs; TIGR00865; bcl-2; 1.
CC PROSITE; PS50062; BCL2_FAMILY; 1.
CC PROSITE; PS01080; BH1; 1.
CC PROSITE; PS01258; BH2; 1.
CC PROSITE; PS01259; BH3; 1.
CC PROSITE; PS01260; BH4_1; 1.
CC PROSITE; PS00063; BH4_2; 1.
CC KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
CC FT DOMAIN 10 30
CC FT DOMAIN 90 104
CC FT DOMAIN 133 152
CC FT DOMAIN 184 199
CC FT TRANSMEM 209 230
CC FT SITE 64 65
CC FT MOD_RES 70 70
CC SQ SEQUENCE 236 AA; 26491 MW; BECADFIEF3337228 CRC64;
Query Match. 40.0%; Score 403; DB 1; Length 236;
Best Local Similarity 35.3%; Pred. No. 3.8e-29;
Matches 92; Conservative 34; Mismatches 64; Indels 52; Gaps 3;
QY 9 DTRALVADPVGYKFKQGY----- 27
D 10 DREIVMYKTHYKLSQRYGVWDVDAAPLGAAPTGIFSFQPSNFTPAVRDVAART 69
QY 28 -----VCGAGFGEPAADPLHQANRAAGDEFTFRFTFSDLAAQLHVTGSAQQRFTQ 81
D 70 SPLRPVATTTGTLSPVPPVHLTLRAGDDFSRRYRSDFAEMSSQLHLPFTARGREAT 129
QY 82 VSDLELFOGPNWGRVLAFFVFGAALCAESVKNEMEPVGVQVQVWVAYLETRADWIHSS 141
D 130 VVEELFRDGVNMGRIVAFFEGGVNMCVSNREMSPLVDNIALMNTYLNRLHHTWIQDN 189
QY 142 GGAAGETALYDGALEARRREGNWSVRTVLTGAVALGALVTGGAFFASK 193
D 190 GGDWDAFVELYG-----PSVRPLDFSWLSLKLTLSSAL-VGACITLGLYLGHK 236

RESULT 15
ID AR11_XENLA STANDARD; PRT; 204 AA.
AC Q91828;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptosis regulator R11 (XR11).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
ON NCBI_TaxID=8355;
RN [1]

```

```
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RA MEDLINE=95331163; PubMed=7607538;
RX Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
RL cell-survival genes.";
RL Gene 158:171-179(1995).
CC -!- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
CC -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -!- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC BRAIN OF MID-METAMORPHIC TO POST-METAMORPHIC TADPOLES AND
CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X82461; CAA57844.1; -.
CC HSP: Q07817; IMAZ.
CC InterPro: IPR000712; Bcl2_BH.
CC InterPro: IPR003093; Bcl2_BH4.
CC InterPro: IPR02475; BCL2_family.
CC InterPro: IPR004725; Bcl2_reg.
CC Pfam: PF00452; Bcl-2; 1.
CC Pfam: PF02180; BH4; 1.
CC SMART: SM00337; BCL; 1.
CC SMART: SM00265; BH4; 1.
CC TIGRfams: TIGR00865; bcl-2; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; 1.
CC PROSITE: PS00062; BCL2_FAMILY; 1.
CC Apoptosis: Transmembrane.
CC DOMAIN 101 120 BH1.
CC FT DOMAIN 152 167 BH2.
CC TRANSMEM 181 198 POTENTIAL.
CC SEQUENCE 204 AA; 23379 MW; 3BFC6B6DDA4CA03 CRC64;
CC -----
Qy Query Match 36.8%; Score 371; DS 1; Length 204;
Db Best Local Similarity 42.1%; Pred.No.2.4e-26;
Qy Matches 82; Conservative 25; Mismatches 62; Indels 26; Gaps 4;
Qy :0 TRALVADFGYKLRQKGVVC-----GAGPGEGPAADPLHQAMR 47
Db :||| ||| ||| ||| :||| :||| :||| :||| :||| :|||
Qy 5 SRDLVERFVSKLSQ-NEACKKFNNNPNFPLMEPTSERPGEGATGIVEEVLQALL 63
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 48 AAGDEFFTRFRRTSDLAQLHVTGPSAQORFTQVSDDELFOGPNMGRLVAVFFVGAALC 107
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 64 EATEEFELRYQRAFDLSLTQLHTQDTAQQSFOQVMGELFRDGTNWGRIVAFPSFGALC 123
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 108 AESVYNKEPLVGQVQEWVAYLETRLDWHSWGWAETALYGDGALAEARLRB--G 165
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 124 VESANKEMTDLLPRIVQMVNLYLEHTLQPMWQENGWGEAFVGLYGNKNAACSRSCRF 183
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 166 NWASVRTVLTCAVAL 180
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 184 RLLTI-VMLTGUFAL 197
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
```

Search completed: October 24, 2003, 10:46:47
Job time : 15.5 secs

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OM protein - protein search, using sw model

Run on: October 24, 2003, 13:43:10 ; Search time 62 Seconds
(without alignments)

803.293 Million cell updates/sec

Title: US-09-925-674A-7

Perfect score: 1007
Sequence: 1 MATPASAPDTRALVADFGV.....LTGAVALGALVTGAFASK 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	996	98.9	193	11	O8996 rattus norv
2	956	94.9	193	11	O8CGL4 mus musculu
3	761	75.6	178	11	O9CYW5 mus musculu
4	761	75.6	178	11	O8CFR2 mus musculu
5	440.5	43.7	233	6	O9MYW4 oryctolagus
6	435.5	43.2	233	11	O35844 mus musculu
7	433.5	43.0	233	6	O8SQ42 felis silve
8	431.5	42.9	233	6	O9N1A2 sus scrofa
9	428.5	42.6	233	6	O9MZS7 ovis aries
10	413	41.0	236	11	O8BQK4 mus musculu
11	403	40.0	238	13	O90Z98 brachydanio
12	401	39.8	180	6	O9BDJ5 bos taurus
13	401	39.8	217	11	O9N3J5 mus musculu
14	399	39.6	236	11	O923R6 cricetus
15	398.5	39.6	180	6	O9BDX7 bos taurus
16	396.5	39.4	235	6	O8I008 felis silve

17	374.5	37.2	188	11	Q9QWX2
18	374.5	37.2	235	11	O35843 mus musculu
19	373.5	37.1	188	4	O9H1R6 homo sapien
20	373	37.0	204	13	Q90ZK2 xenopus lae
21	354	35.2	185	6	O8MU81 bos taurus
22	347	34.5	219	11	Q9N336 mus musculu
23	343.5	34.1	199	11	Q8C5P0 mus musculu
24	296	29.4	89	13	O8UWJ1 gallus gall
25	189	18.8	209	13	O9JK59 rattus norv
26	185	18.4	170	11	O9MU15 rattus norv
27	184	18.3	209	11	O8C264 mus musculu
28	176.5	17.5	192	13	Q929N4 brachydanio
29	175.5	17.4	190	4	O8NFF3 homo sapien
30	171.5	17.0	221	13	Q98U13 xenopus lae
31	168.5	16.7	125	4	O9H1R5 homo sapien
32	163	16.2	58	11	O9R1B3 rattus norv
33	162	16.1	235	5	O967D2 geodia cydo
34	159.5	15.8	163	6	O9MZS6 ovis aries
35	155.5	15.4	173	11	O8K3J2 mus musculu
36	153	15.2	173	4	O8WZ49 homo sapien
37	153	15.2	173	11	Q9JKL3 rattus norv
38	152	15.1	67	6	O8MJ33 cervus elap
39	148.5	14.7	218	5	O9N754 subarites d
40	148	14.7	192	6	O8SQ43 felis silve
41	147	14.6	192	6	O8HYU5 canis fami
42	146.5	14.5	179	4	O9NYG7 homo sapien
43	144	14.3	149	6	O9GMG7 ovis aries
44	143	14.2	177	13	Q90ZK1 gallus gall
45	142.5	14.2	179	12	Q951F2 meleagrid h

ALIGNMENTS

RESULT 1

O8996
ID O8996 PRELIMINARY; PRT; 193 AA.
AC O8996;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Bcl-w.
DE Bcl-w.
GN BCL-W.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=93292146; PubMed=10366024;
RA Hamner S... Skoglosa Y... Lindholm D.;
RT "Differential expression of bcl-w and bcl-x messenger RNA in the
developing and adult rat nervous system.";
RL Neuroscience 91:673-684(1993).
DR EMBL; AF096291; AAC64200.1; -.
DR HSSP; Q07817; 1WAZ.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 193 AA; 20620 MW; 36D6742F4529AFB4 CRC64;

Query Match 98.9%; Score 996; DB 11; Length 193;
Best: Local Similarity 98.4%; Pred. No. 2.9e-81;

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Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADVGVYKLRQKGVYCGAGGEGPAADPLHQAMRAAGDEFEFRRT 60
   |||||
Db 1 MATPASTPDTRALVADVGVYKLRQKGVYCGAGGEGPAADPLHQAMRAAGDEFEFRRT 60
   |||||

QY 61 FSDLAALQHVTPGSAOQRFTQVSDLELFGGPNWGRVAFVFGAALCAESVKNEMEPLVG 120
   |||||
Db 61 FSDLAALQHVTPGSAOQRFTQVSDLELFGGPNWGRVAFVFGAALCAESVKNEMEPLVG 120
   |||||

QY 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYDGALEEARLRGNWASVRTVLTCAVAL 180
   |||||
Db 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYDGALEEARLRGNWASVRTVLTCAVAL 180
   |||||

QY 181 GALVTVGGAFFASK 193
   |||||
Db 181 GALVTVGGAFFASK 193
   |||||

RESULT 2
Q8CGL4 PRELIMINARY; PRT; 193 AA.
ID Q8CGL4 AC
AC Q8CGL4 AC
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Bcl2-like protein 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC "Extraction from neonatal mouse skin after IGF-1 stimulation."
RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY703444; AA013177.1; -.
SQ SEQUENCE 193 AA; 29950 MW; 258AC1818166DFA0 CRC64;

Query Match 94.9%; Score 956; DB 11; Length 193;
Best Local Similarity 95.3%; Pred. No. 1.1e-77;
Matches 184; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADVGVYKLRQKGVYCGAGGEGPAADPLHQAMRAAGDEFEFRRT 60
   |||||
Db 1 MATPASTPDTRALVADVGVYKLRQKGVYCGAGGEGPAADPLHQAMRAAGDEFEFRRT 60
   |||||

QY 61 FSDLAALQHVTPGSAOQRFTQVSDLELFGGPNWGRVAFVFGAALCAESVKNEMEPLVG 120
   |||||
Db 61 FSDLAALQHVTPGSAOQRFTQVSDLELFGGPNWGRVAFVFGAALCAESVKNEMEPLVG 120
   |||||

QY 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYDGALEEARLRGNWASVRTVLTCAVAL 180
   |||||
Db 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYDGALEEARLRGNWASVRTVLTCAVAL 180
   |||||

QY 181 GALVTVGGAFFASK 193
   |||||
Db 181 GALVTVGGAFFASK 193
   |||||

RESULT 3
Q9CYW5 PRELIMINARY; PRT; 178 AA.
ID Q9CYW5 AC
AC Q9CYW5 AC
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Bcl2-like 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Eye;

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ichii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yaranaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bernaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 403:685-690(2001).
DR EMBL; AK013244; BAB28740.1; -.
DR HSSP; Q07817; IMAZ.
DR MGD; MGI:108052; Bcl2l2.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SMC0337; BCL; 1.
DR SMART; SMC0265; BH4; 1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS00063; BH4_2; 1.
DR PROSITE; PS00063; BH4_2; 1.
SQ SEQUENCE 178 AA; 19147 MW; E2D4C3F79528E9D7 CRC64;

Query Match 75.6%; Score 761; DB 11; Length 178;
Best Local Similarity 95.3%; Pred. No. 2.7e-60;
Matches 143; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADVGVYKLRQKGVYCGAGGEGPAADPLHQAMRAAGDEFEFRRT 60
   |||||
Db 1 MATPASTPDTRALVADVGVYKLRQKGVYCGAGGEGPAADPLHQAMRAAGDEFEFRRT 60
   |||||

QY 61 FSDLAALQHVTPGSAOQRFTQVSDLELFGGPNWGRVAFVFGAALCAESVKNEMEPLVG 120
   |||||
Db 61 FSDLAALQHVTPGSAOQRFTQVSDLELFGGPNWGRVAFVFGAALCAESVKNEMEPLVG 120
   |||||

QY 121 QVQEMWVAYLETRLADWIHSSGGWAEFTAL 150
   |||||
Db 121 QVQDMWVAYLETRLADWIHSSGGWVRSSQL 150
   |||||

RESULT 4
Q8CFR2 PRELIMINARY; PRT; 178 AA.
ID Q8CFR2 AC
AC Q8CFR2 AC
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Bcl2-like 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Eye;

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RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
SQ EMBL; BCC40369; AAH43369.1; -;
SEQUENCE 178 AA; 191:9 MW; E2C3F3F79528E9D7 CRC64;

Query Match 75.6%; Score 76.; DB 11; Length 178;
Best Local Similarity 95.3%; Pred. No. 2.7e-60;
Matches 143; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 NATPASADTRALVADFGYKLRQKGYVCGAGPGEPAADPLHQAMPAAGDEFETRFRRT 60
DB 1 NATPASADTRALVADFGYKLRQKGYVCGAGPGEPAADPLHQAMPAAGDEFETRFRRT 60
QY 61 FSDLAQAQLHVTGSGAQQCTQVDSJLFGGPNWGRNLVAFVFGAALCAESVNKMEPLVG 120
DB 61 FSDLAQAQLHVTGSGAQQCTQVDSJLFGGPNWGRNLVAFVFGAALCAESVNKMEPLVG 120
QY 121 QVCEWVAYLETR-ADWIHSSGGWAEFTAJ 150
DB 121 QVCEWVAYLETR-ADWIHSSGGWAEFTAJ 150

RESULT 5
Q9MYW4 PRELIMINARY; PRT; 233 AA.

AC Q9MYW4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Bcl-X.
OS Oryctolagus cuniculus (Rabbit)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Knott J.C., Robertson L., James E.R.;
RT "Rabbit Bcl-X";

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY005131; AAF88137.1; -;
DR HSSP; P53563; 1AF3.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01360; BH4; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;

Query Match 43.7%; Score 440.5; DB 6; Length 233;
Best Local Similarity 42.0%; Pred. No. 1.7e-31;
Matches 94; Conservative 22; Mismatches 57; Indels 51; Gaps 4;

QY 11 RALVADFVGYKLRQKGYVCGAGPGEPAADPLHQAMPAAGDEFETRFRRT 39
DB 6 RELVDFLSYKLSQKGSQVSDVEENRTEAPEETEAETPSAINGNPWHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFETRFRRTSDLAQAQLHVTGSGAQQCTQ 81
DB 66 NCATGSSSLDAREVIPMTAVKQALREAGDEFELRYRAFSDLTSQCHITPGTAYQSFEQ 125
QY 82 VSDLELFOGGPNWGRNLVAFVFGAALCAESVNKMEPLVGQVQEWVAYLETRLDWIHSS 141
DB 126 VVNELFRDGVNMGRIVAFFSFGGALCVESVDKEMQVLVSR-IAAWKATYLNDFLEPFIQEN 185

QY 142 GQWABFTALYGDGALEEARLRRE--GNWASVRTVLTGVALCAL 183
DB 186 GQWDTFVELYGNNAAESRKQGERNRWFLTGMTVAGVLLGSL 229
RESULT 6
C35844 PRELIMINARY; PRT; 233 AA.

AC C35844;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Bcl-X.
GN SCL2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10390;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=86/CBA; TISSUE=Thymus;
RX MEDLINE=98051053; PubMed=9390687;
RA Yang X.-F., Weber G.F., Cantor H.;
RT "A novel Bcl-x isoform, connected to the T cell receptor regulates apoptosis in T cells";
RL Immunity 7:629-639(1997).
DR EMBL; U51278; AAC53459.1; -;
DR HSSP; P53563; 1AF3.
DR MGD; MGI:88139; Bcl2L.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01360; BH4; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 233 AA; 26033 MW; 3083FD8327E072E CRC64;

Query Match 43.2%; Score 435.5; DB 11; Length 233;
Best Local Similarity 41.8%; Pred. No. 4.8e-31;
Matches 94; Conservative 22; Mismatches 56; Indels 53; Gaps 4;

QY 11 RALVADFVGYKLRQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRTSDLAQAQLHVTGSGAQQCTQ 28
DB 6 RELVDFLSYKLSQKGSQVSDVEENRTEAPEETEAETPSAINGNPWHLADSPAV 65
QY 29 CGAGPGEPAAD-----PLHQAMRAAGDEFETRFRRTSDLAQAQLHVTGSGAQQCTQ 90
DB 66 NCA-TGHSLSLDAREVIPMAAVKQALREAGDEFELRYRAFSDLTSQCHITPGTAYQSFE 124
QY 81 QVSDLELFOGGPNWGRNLVAFVFGAALCAESVNKMEPLVGQVQEWVAYLETRLDWIHSS 140
DB 125 QVNELFRDGVNMGRIVAFFSFGGALCVESVDKEMQVLVSR-IAAWKATYLNDFLEPFIQEN 184
QY 141 SCGWAEFTALYGDGALEEARLRREG--NWSVRTVLTGVALCAL 183
DB 185 NGQWDTFVDLYGNNAAESRKQGERNRWFLTGMTVAGVLLGSL 229

RESULT 7
Q8SQ42 PRELIMINARY; PRT; 233 AA.

ID Q8SQ42
AC Q8SQ42;
DT 01-JUN-2002 (TREMBLrel. 21, Created)

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DT 01-JUN-2002 (TrEMBLrel. 2; Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22; Last annotation update)
DE BCL-XL protein.
GN BCL-XL
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
CN NCBI_TaxID=9685;
[1]
SEQUENCE FROM N.A.
RA Nagafuchi S., Sano J., Kano R., Hasegawa A.;
RT "Molecular cloning of feline Bcl-2 family.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AB080951; BAB85856.2; -.
DR InterPro: IPR000112; BCL2_BH.
DR InterPro: IPR003093; BCL2_FAMILY.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR004725; BCL2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1; 1.
DR PROSITE: PS0063; BH4_2; 1.
DR PROSITE: PS0063; BH4_2; 1.
SQ SEQUENCE 233 AA; 26047 MW; 2FA312818B25E17D CRC64;

Query Match 42.9%; Score 431.5; DB 6; Length 233;
Best Local Similarity 41.8%; Pred. No. 1.1e-30;
Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADPVGKLRQKGY-----V 28
DB 6 RELVDFLSYKLSQKGYSWQFTDVENRTEAPGCTESEAEETPSAINGNPSWHLADSPAV 65

QY 29 CGAGPGEPAAD-----PLHQAMRAAGDEFTFRFTFSLAAQLHVTGPSAQORFT 80
DB 66 NGA-TGHSSSLDAREVIPAAMVKQALREAGDEFELRYRRAFSDLTSQLHTPGTAYQSFE 124

QY 81 QVSDLEFQGGPNWGRVAFVFGAALCAESVNKEMEPVGVQVEMVAYLETRLDWHS 140
DB 125 QVNVLEFRDGVNWGRVAFVFGAALCAESVNKEMEPVGVQVEMVAYLETRLDWHS 184

QY 141 SGWMAEFTALYGDGALBEARRLRD--GNWASVVRTVLTGVALGAL 183
DB 185 NGGWDTFVELYGNNAAESRKQGERFNRWELTGMTLAGVVLGSL 229

RESULT 9
Q9MZS7
ID Q9MZS7 PRELIMINARY; PRT; 233 AA.
AC Q9MZS7
DT 01-OCT-2002 (TrEMBLrel. 15; Created)
DT 01-OCT-2000 (TrEMBLrel. 15; Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21; Last annotation update)
DE Bcl-x long protein.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
CN NCBI_TaxID=9940;
[1]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;
RT "Bcl-x in the sheep ovary.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF164517; AAF89532.1; -.
DR HSSP; P53563; 1AF3.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; BCL2_FAMILY.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR004725; BCL2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1; 1.
DR PROSITE; PS0063; BH4_2; 1.
DR PROSITE; PS0063; BH4_2; 1.

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DR PROSITE; PS50063; BH4 2; 1.
SQ SEQUENCE 233 AA; 26134 MW; 012BFA1382762915 CRC64;

Query Match 42.6%; Score 428.5; DB 6; Length 233;
Best Local Similarity 40.6%; Pred. No. 2e-30; Indels 51; Gaps 4;
Matches 91; Conservative 23; Mismatches 59;

QY 11 RALVADFVGYKLRQKGY-----VCGAGP-----GEGPAA 39
DB 6 RELVVDVFLSYKLKSGYSGFSQSDVEENRTEAPEGTESDMETPSAINGNFWHLADSPAV 65

QY 40 D-----PLHCANRAGCDEFEFRTRTFSDLAQLHVTTPGSAQQR 81
DB 66 NGATGSHSLDAREVIPMAVKQALREAGDEFELRYRRAFSDLTSQHTTPGTAYQSFQ 123

QY 82 VSEDLFOGGPNWGRUVAFFVFGAALCAESVKNKEMPLVGQVQVQVWVAYLETRLADWHS 141
DB 126 VVNELFROGVNWRIVAFSFGGALCVESVQKQVLSRATWATYLNHDLHPN-CEN 185

QY 142 GWAEEFTLYDGALEAEARRURE--GNWASVTVLTGAVAGAL 183
DB 186 GGMWTFVELYGNNAAESRQKQERENRWFELTGM-VAGVVLGSL 229

RESULT 10
Q8BQK4 PRELIMINARY; PRT; 236 AA.
AC Q8BQK4;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE B-cell leukemia/lymphoma 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK049473; BAC33767.1; -.
SQ SEQUENCE 236 AA; 26437 MW; B726BFA3AA1C718 CRC64;

Query Match 41.0%; Score 413; DB 11; Length 236;
Best Local Similarity 37.5%; Pred. No. 5e-29; Indels 52; Gaps 5;
Matches 87; Conservative 34; Mismatches 59;

QY 9 DTRALVADPVGKLRQKGYVCGAG-----PG----- 34
DB 10 DNREIVMKYIHYKLSQGYEWMDAGDAADAPLGAAPTC:FSQPESNPNPAVHRDXAART 69

QY 35 -----EGPAAEP-----LHCANRAGCDEFEFRTRTFSDLAQLHVTTPGSAQQR 81
DB 70 SPLRLPVATTGALSPVPVPHVLTLLRRAGDDPSRYYRSDFAEMSSQLHRTFTARGRFAT 129

QY 82 VSEDLFOGGPNWGRUVAFFVFGAALCAESVKNKEMPLVGQVQVQVWVAYLETRLADWHS 141
DB 130 VVEELFRGVNWRIVAFSFGGALCVESVQKQVLSRATWATYLNHDLHPN-CEN 189

QY 142 GWAEEFTLYDGALEAEARRUREGNWASVTVLTGAVAGALVTVGAFASK 193
DB 190 GGMWDAFVELY----PSMRPLFDPSMLSLKLTLSDAL-VGACITLGLAYLGK 236

RESULT 11
Q90298 PRELIMINARY; PRT; 238 AA.
AC Q90298;

Query Match 40.0%; Score 403; DB 13; Length 238;
Best Local Similarity 36.6%; Pred. No. 4e-28;
Matches 87; Conservative 27; Mismatches 62; Indels 62; Gaps 6;

QY 11 RALVADFVGYKLRQKGYC-----GAG----- 32
DB 6 RELVVFYKLSQRNYPCNHGLTETNRTDGAENGEGAGAGATTLVNGTNRNAST 65

QY 33 --PGEPAADPLHQ-----AMRAAGDEFETRFRTRTFSDLAQLHVTTPGSAQQR 78
DB 66 GTTPQSPASSPQRTNGSGGLDVAKEALRDSANEFELYSRAFNDSLSQLHITPATYQS 125

QY 79 FTQVDELFOGGPNWGRUVAFFVFGAALCAESVKNKEMPLVGQVQVQVWVAYLETRLADW 138
DB 126 FESVMDVEFRDGVNWRIVGLFAGGALCVCEKEMSPVLGRIAEWMTVYLDNHQPMI 185

QY 139 HSGGWAEEFTLYDGALEAEARRURE--NWA-SVRTVLTGAVAGALVTVGAFASK 193
DB 186 QGQGGWERFAEIFGKDAAESRKSQESPKKMLFAGMTLLTG-----VVVGGGLIAQK 236

RESULT 12
Q93DD5 PRELIMINARY; PRT; 180 AA.
ID Q93DD5;
AC Q93DD5;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Anti-apoptotic regulator Bcl-xL (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Amills M., Bouzat J.;
RT "Characterization of the bovine bcl-xL gene and related pseudogenes.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF245488; AAK31307.1; -.
DR EMBL; AF245489; AAK31308.1; -.
DR HSSP; Q07817; 1MAZ.
DR InterPro; IPR000712; Bcl2_BH.
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DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
FT NON_TER 1
FT NON_TER 180
SQ SEQUENCE 180 AA; 20062 YW; 95DC436F95DABDA6 CRC64;

Query Match 39.8%; Score 401; DB 6; Length 180;
Best Local Similarity 53.5%; Pred. No. 4.2e-28;
Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;

QY 44 QAMRAAGDEFETRRPTESDLAAQLHVTGSAQOQFTQVSDLPFGGPNWGRVAFVFG 103
DB 38 QALREAGDEFELRYRAESDLTSQLHTPGTAYQSFQVNVNELPRDGVNNGRIVAFPSFG 97
QY 104 AALCAESVNKMEPLVGQVQEMWVAYLETRLADWIHSSGGNAEFTALYGDGALEAPRLR 163
DB 98 GALCVESVDKEMQVLVSRIATWATYLNHLEPWIQENGWDTFVELYGNNAAESRKQ 157
QY 164 E--GNWASVRTVLTCAVALGAL 183
DB 158 ERFNWFMTGMTVAGVLLGSL 179

RESULT 13
Q99N35 PRELIMINARY; PRT; 217 AA.
AC Q99N35;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE B-cell leukemia/lymphoma x (Fragment).
GN BCLX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Yang X.-F., Cantor H.;
RT "Novel cDNA structure and genomic organization of apoptosis regulatory
RT gene Bcl-x-Gamma."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF133282; AAK15455.1;
DR EMBL; AF133281; AAK15455.1; JOINED.
DR HSSP; P53563; 1AF3.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS00963; BH4-2; 1.
SQ SEQUENCE 217 AA; 24234 MW; 3B5A4E809A7DEF18 CRC64;

Query Match 39.8%; Score 401; DB 11; Length 217;
Best Local Similarity 53.5%; Pred. No. 5.4e-28;
Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;

QY 44 QAMRAAGDEFETRRPTESDLAAQLHVTGSAQOQFTQVSDLPFGGPNWGRVAFVFG 103
DB 72 QALREAGDEFELRYRAESDLTSQLHTPGTAYQSFQVNVNELPRDGVNNGRIVAFPSFG 131
QY 104 AALCAESVNKMEPLVGQVQEMWVAYLETRLADWIHSSGGNAEFTALYGDGALEAPRLR 163
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DB 132 GALCVESVDKEMQVLVSRIASWATYLNHLEPWIQENGWDTFVELYGNNAAESRKQ 192
QY 164 E--GNWASVRTVLTCAVALGAL 183
DB 192 ERFNWFMTGMTVAGVLLGSL 213

RESULT 14
Q923R6 PRELIMINARY; PRT; 236 AA.
AC Q923R6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE B-cell lymphoma protein 2.
GN BCL2.
OS Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
CC Cricetulus.
CX NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RA Lai D.Z., Chen W., Wang H.T.;
RT "Construction of a robust CHO cell line for biopharmaceutical use."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF404339; AAK92201.1;
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR004725; Bcl-2; 1.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS00963; BH4-2; 1.
SQ SEQUENCE 236 AA; 26500 MW; BEDF052EF32CA8B8 CRC64;

Query Match 39.6%; Score 399; DB 11; Length 236;
Best Local Similarity 35.3%; Pred. No. 9e-28;
Matches 82; Conservative 32; Mismatches 66; Indels 52; Gaps 3;

QY 9 DTRALVADPVGKLRQKCY-----
DB 10 DNRLEIMKVIYIKUSQRYEWDVGVDNAPLGAAPTQCFISFQPSNPPTPAVHEDMAART 69
QY 28 -----VCGAGPGEPAADPLHQAMRAAGDEFETRRPTESDLAAQLHVTGSAQOQFTQ 81
DB 70 SPLRPIVATTGTLSPVPVVLTLRRAGDDFSRRYRDRDFAEMSSQLHLTPTTARGFAT 129
QY 82 VSELPFGGPNWGRVAFVFGSAALCAESVNKMEPLVGQVQEMWVAYLETRLADWIHSS 141
DB 130 VVEELFRDGVNNGRIVAFVFEFGVNCVSVNREMSPLVDNIALNMTEYLNPHLHTWQDN 189
QY 142 GGWAETALYGDGALEAEARRLEGWASVRTVLTCAVALGALVTVGAFVASK 193
DB 190 GGWDAFVELYG----PSVRPLDFSWLSLXTLLNLAL-VGACITLGYLGHK 236

RESULT 15
Q9BDX7 PRELIMINARY; PRT; 180 AA.
AC Q9BDX7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Search completed: October 24, 2003, 10:51:07
Job time : 67 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:03:45 ; Search time 1737.99 Seconds
(without alignments)
13722.924 Million cell updates/sec

Title: US-09-925-674A-6
Perfect score: 583
Sequence: 1 atggcgaccacgcctcggc.....cttttttctagcaagtga 583

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2889711 seqs, 20454913396 residues

Total number of hits satisfying chosen parameters: 577422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba:

2: gb_hgt:

3: gb_in:

4: gb_om:

5: gb_ov:

6: gb_pat:

7: gb_ph:

8: gb_pl:

9: gb_pr:

10: gb_ro:

11: gb_sta:

12: gb_sy:

13: gb_un:

14: gb_vi:

15: em_ba:

16: em_fun:

17: em_hum:

18: em_in:

19: em_mu:

20: em_om:

21: em_or:

22: em_ov:

23: em_pat:

24: em_ph:

25: em_pl:

26: em_ro:

27: em_sta:

28: em_un:

29: em_vi:

30: em_hgt_hum:

31: em_hgt_inv:

32: em_hgt_other:

33: em_hgt_mus:

34: em_hgt_pln:

35: em_hgt_rod:

36: em_hgt_tam:

37: em_hgt_vrt:

38: em_sy:

39: em_hgtc_hum:

40: em_hgtc_mus:

41: em_hgtc_other:

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	582	99.8	582	6	AX481423	AX481423 Sequence
2	582	99.8	582	9	HSU59747	U59747 Human Bcl-w
3	579.8	99.5	3542	9	D87462	D87461 Human: mRNA
4	578.2	99.2	583	6	AX022529	AX022529 Sequence
5	578.2	99.2	583	6	AX030817	AX030817 Sequence
6	578.2	99.2	1437	9	BC021198	BC021198 Homo sapi
7	572.6	98.2	579	6	AR020780	AR020780 Sequence
8	532.4	91.3	582	10	AF096291	AF096291 Rattus no
9	527.8	90.5	579	6	AR020779	AR020779 Sequence
10	527.6	90.5	582	10	MMU55746	U59746 Mus muscu
11	527.6	90.5	3476	10	AF030769	AF030769 Mus muscu
12	516.4	88.6	3473	10	AY170344	AY170344 Mus muscu
13	505.8	86.8	581	6	AX022531	AX022531 Sequence
14	505.8	86.8	581	6	AX030819	AX030819 Sequence
15	446	76.5	220818	2	AC128940	AC128940 Rattus no
16	446	76.5	223933	2	AC097389	AC097389 Rattus no
17	428.8	73.6	1098	6	BD078624	BD078624 Human chr
18	428.2	73.4	196292	9	CNS0003B	AL049825 Human chr
19	398.6	66.7	148278	2	AC079885	AC079885 Rattus no
20	398.6	66.7	180665	2	AC084240	AC084240 Rattus no
21	388.6	66.7	221557	2	AC134055	AC134055 Rattus no
22	386.6	66.3	210784	2	AC119293	AC119293 Rattus no
23	386.6	66.3	263901	2	AC115371	AC115371 Rattus no
24	380.2	65.2	3815	10	BC040369	BC040369 Mus muscu
25	380.2	65.2	237561	10	AC116591	AC116591 Mus muscu
26	257	44.1	6049	6	AX345130	AX345130 Sequence
27	239.8	41.1	749	5	XLR1	X82462 X.laavis R1
28	223	38.3	6049	6	AX345131	AX345131 Sequence
29	143	24.5	764	10	RNU10579	U10579 Rattus norv
30	143	24.5	1742	6	BD012974	BD012974 A mutagen
31	143	24.5	1742	6	BD013799	BD013799 Modified
32	143	24.5	1742	10	RNU72350	U72350 Rattus norv
33	143	24.5	2232	10	RNCBLXLS	X82537 R.norvegicu
34	142.2	24.4	1252	4	AB073983	AB073983 Canis fam
35	140.6	24.1	1163	4	AB080951	AB080951 Felis cat
36	139.2	23.9	702	4	AY005131	AY005131 Oryctolag
37	138.2	23.7	726	10	RNU34963	U34963 Rattus norv
38	138.2	23.7	726	10	S76513	S76513 bcl-x-apopt
39	135.8	23.3	766	4	AF164517	AF164517 Ovis arie
40	135.6	23.3	720	4	AF216205	AF216205 Sus scrof
41	135.6	23.3	752	4	SSJ001203	AJ001203 Sus scrof
42	134.2	23.0	541	4	AF245488	AF245488 Bos tauru
43	133.8	23.0	695	6	AX525912	AX525912 Sequence
44	132.8	22.8	699	10	MMBCLXL	X83574 M.musculus
45	132.8	22.8	702	10	MMU10101	U10101 Mus muscu

ALIGNMENTS

RESULT 1	AX481423	Sequence	582 bp	DNA	linear	PAT 16-AUG-2002
LOCUS	AX481423	Sequence	37 from Patent WO02055693.			
DEFINITION	AX481423	Sequence	37 from Patent WO02055693.			
ACCESSION	AX481423	Sequence	37 from Patent WO02055693.			
VERSION	AX481423.1	GI:22316337				
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
REFERENCE	1	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Kreutzer, R., Limmer, S., Rost, S. and Hadwiger, F.					
TITLE	Method for inhibiting the expression of a target gene					
JOURNAL	Patent: WO 02055693-A 37 18-JUL-2002;					

Pred. No. is the number of results predicted by chance to have a

Ribopharma AG (DE)		Location/Qualifiers	
source		1..582	
		/organism="Homo sapiens"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:9606"	
BASE COUNT	104 a	156 c	211 g
ORIGIN	111 t		
Query Match 99.8%; Score 582; DB 6; Length 582;			
Best Local Similarity 100.0%; Pred. No. 1.2e-120;			
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGGGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT	60
DB	1	ATGGGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT	60
QY	61	AGCTGAGCAGAGAGGTTATGTCTGTGAGCTGGCCCCGGGAGGCCCCAGCAGCTGAC	120
DB	61	AGCTGAGGAGAGAGGTTATGTCTGTGAGCTGGCCCCGGGAGGCCCCAGCAGCTGAC	120
QY	121	CGCTGACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCGGTTCCGGCGCACC	180
DB	121	CGCTGACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCGGTTCCGGCGCACC	180
QY	181	TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCACGACGCTTCA	240
DB	181	TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCACGACGCTTCA	240
QY	241	CAGGTCTCGACGAACTTTTCAAGGGGCCCCAACTGGGCGGCTTGTAGCCTTCTTT	300
DB	241	CAGGTCTCGACGAACTTTTCAAGGGGCCCCAACTGGGCGGCTTGTAGCCTTCTTT	300
QY	301	GTCTTTGGGCTGCACTGTGTCTGAGAGTGTCAACAGGAGATGGAACCACTGGTGGGA	360
DB	301	GTCTTTGGGCTGCACTGTGTCTGAGAGTGTCAACAGGAGATGGAACCACTGGTGGGA	360
QY	361	CAAGTCAGAGAGTGGATGTGCTACCTGAGAGACCGGCTGGCTGAGTCCACAGC	420
DB	361	CAAGTCAGAGAGTGGATGTGCTACCTGAGAGACCGGCTGGCTGAGTCCACAGC	420
QY	421	AGTGGGGCTGGCGAGTTCACAGCTCTATACGGGGACGGGCGCTGGAGAGCGCGG	480
DB	421	AGTGGGGCTGGCGAGTTCACAGCTCTATACGGGGACGGGCGCTGGAGAGCGCGG	480
QY	481	CGTCTCGGAGAGGAACTGGGCACTAGTGAGGACAGTGTGACGGGGCGCTGGCACTG	540
DB	481	CGTCTCGGAGAGGAACTGGGCACTAGTGAGGACAGTGTGACGGGGCGCTGGCACTG	540
QY	541	GGGGCCCTGGTAAGTGTAGGGCCCTTTTGTAGCAAGTGA	582
DB	541	GGGGCCCTGGTAAGTGTAGGGCCCTTTTGTAGCAAGTGA	582
RESULT 2			
HSU59747			
LOCUS	582 bp mRNA linear PRI 29-SEP-1996		
DEFINITION	Human Bcl-w (bcl-w) mRNA, complete cds.		
ACCESSION	U59747		
VERSION	U59747.1 GI:1572492		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 582)		
AUTHORS	Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G., Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.		
TITLE	bcl-w, a novel member of the bcl-2 family, promotes cell survival		
JOURNAL	Oncogene 13 (4), 665-675 (1996)		
MEDLINE	96358615		
PUBMED	8761287		
REFERENCE	2 (bases 1 to 582)		

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RESULT 3
D87461
LOCUS       D87461             3542 bp    mRNA             linear           PR: 06-OCT-2001
DEFINITION Human mRNA for KIAA0271 gene, complete cds.
ACCESSION   D87461
VERSION     D87461.1   GI:1944417
KEYWORDS    KIAA0271,
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Nagase,T., Seki,N., Ishikawa,K., Chitara,M., Kawarabayashi,Y.,
            Chara,O., Tanaka,A., Kozani,H., Miyajima,N. and Nomura,N.
            Prediction of the coding sequences of unidentified human genes. VI
            The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
            analysis of cDNA clones from cell line KG-1 and brain
            DNA Res. 3 (5), 321-329 (1996)
JOURNAL     97191544
MEDLINE     9039502
PUBMED      9039502
REFERENCE   2 (bases 1 to 3542)
AUTHORS     Chara,O., Nagase,T., Kikuno,R. and Nomura,N.
            Direct Submission
TITLE       Submitted (27-AUG-1996) Osamu Chara, Kazusa DNA Research Institute,
            1532-3, Yana, Kisarazu, Chiba 292-0612, Japan
            (E-mail:cdnainfo@kazusa.or.jp, Tel: +81-439-52-3913)
            Location/Qualifiers
FEATURES             1..3542
                    /organism="Homo sapiens"
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                    /db_xref="taxon:9606"
                    /clone="HA6752"
                    /sex="male"
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                    /cell_type="myoblast"
                    /tissue_type="brain"
                    /clone_lib="pSPORT 1"
                    /gene="KIAA0271"
                    /rname="KIAA0271"
                    /size=177
                    /note="similar to human transforming protein bcl-2
                    (A24428)"
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                    /protein_id="BAAL9666.1"
                    /db_xref="GI:1944418"
                    /translation="MATPASADPTRALVADFGYKLRQYVCGAGPGEGPAADPLHQ
                    AMRAGDEPFRFRFTFSDLAOLHVTGSAQORFTQVSDLEFQGGPNMGRVAFVFLF
                    GAALCAESVNKEMEPVGVQEMVAYLETRLDVHSHSGGWAFFALYGGGALEEAR
                    RLREGNWSVRTVLGTGALVALVTGGAFFASK"
BASE COUNT      804 a   817 c   1030 g   891 t
ORIGIN
Query Match      99.5%;   Score 579.8;   DB 9;   Length 3542;
Best Local Similarity 99.7%;   Pred. No. 2.9e-120;
Matches 581;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACCGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
DB 177 ATGGCGACCCAGCCTCGGCCCCAGACACACCGGGCTCTGGTGGCAGACTTTGTAGTTAT 236
QY 61 AAGCTGAGGAGAGAGGTTATGCTGTGGAGCTGGCCCGGGAGGGCCAGACGCTGAC 120
DB 237 AAGCTGAGGAGAGAGGTTATGCTGTGGAGCTGGCCCGGGAGGGCCAGACGCTGAC 296
QY 121 CCGTGCACCAAGCCATGCGGGGAGCTGGAGATGAGTTGAGACCCCGCTTCGGGGCCACC 180
DB 297 CCGTGCACCAAGCCATGCGGGGAGCTGGAGATGAGTTGAGACCCCGCTTCGGGGCCACC 356
QY 181 TTCTCTGATCTGGGGCTCAGCTGATGATGACCCCGAGCTTCCAGCCAGCAACGCTTACC 240
DB 357 TTCTCTGATCTGGGGCTCAGCTGATGATGACCCCGAGCTTCCAGCCAGCAACGCTTACC 416

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QY 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCGGCTTGTAGCCTTCTTT 300
DB 417 CAGGCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCGGCTTGTAGCCTTCTTT 476
QY 301 GTCTTTGGGGCTGCACCTGTGTGCTGTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
DB 477 GTCTTTGGGGCTGCACCTGTGTGCTGTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 536
QY 361 CRAAGTCAGAGAGTGAATGCTGGCTTACCTGGAGACGCGGCTGGTGAAGTCCAGAC 420
DB 537 CAAGTCAGAGAGTGAATGCTGGCTTACCTGGAGACGCGGCTGGTGAAGTCCAGAC 596
QY 421 AGTGGGGCTGGGGGAGTTCACAGCTCTATACGGGGACGGGGCTTGGAGAGCGGG 480
DB 597 AGTGGGGCTGGGGGAGTTCACAGCTCTATACGGGGACGGGGCTTGGAGAGCGGG 656
QY 481 CGTCTCGGGAGGGGAACCTGGGCACTCAGTGAGGACAGTGTCTACGGGGGCGCTGGCCTG 540
DB 657 CGTCTCGGGAGGGGAACCTGGGCACTCAGTGAGGACAGTGTCTACGGGGGCGCTGGCCTG 716
QY 541 GGGGGCTCTGTAAGTCTAGGGGCTTTTGTGTAGCAAGTGAA 583
DB 717 GGGGGCTCTGTAAGTCTAGGGGCTTTTGTGTAGCAAGTGAA 759

RESULT 4
AX022529
LOCUS       AX022529             583 bp    DNA             linear           PAT 27-SEP-2000
DEFINITION Sequence 6 from Patent EP0932674.
ACCESSION   AX022529
VERSION     AX022529.1   GI:10046125
KEYWORDS
SOURCE      unidentified
            unclassified.
REFERENCE   1
AUTHORS     Adams,J.M., Holmgren,S.P., Cory,S. and Gibson,J.M.
            A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
            apoptosis-controlling genes
            Patent: EP 0932674-A 6 04-AUG-1999;
            AMRAD OPERATIONS PTY LTD (AU)
FEATURES             1..583
                    /organism="unidentified"
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                    /db_xref="taxon:32644"
                    /note="unnamed protein product"
                    /codon_start=1
                    /protein_id="CAC07880.1"
                    /db_xref="GI:10046126"
BASE COUNT      105 a   157 c   210 g   111 t
ORIGIN
Query Match      99.2%;   Score 578.2;   DB 6;   Length 583;
Best Local Similarity 99.5%;   Pred. No. 8.5e-120;
Matches 580;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY 1 ATGGGACCCAGCCTCGGCCCCAGACACACCGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
DB 1 ATGGGACCCAGCCTCGGCCCCAGACACACCGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
QY 61 AAGCTGAGGAGAGGTTATGCTGTGGAGCTGGCCCGGGAGGGCCAGACGCTGAC 120
DB 61 AAGCTGAGGAGAGGTTATGCTGTGGAGCTGGCCCGGGAGGGCCAGACGCTGAC 120
QY 121 CCGCTGCACCAAGCCATGCGGGGAGCTGGAGATGAGTTGAGACCCCGCTTCCGGGGCACC 180

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Db      121  CCGCTGCACCAAGCCATCGCGGACGCTGGAGATGAGTTGAGACCCCGCTTCGGCGCACC 180
QY      181  TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCACGACCAACGCTTCACC 240
Db      182  TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCACGACCAACGCTTCACC 240
QY      241  CAGGTCTCCGACGAACCTTTTCAAGGGGCCCCAACTGGGCGGCTTGTAGCCCTTCCT 300
Db      241  CAGGTCTCCGACGAACCTTTTCAAGGGGCCCCAACTGGGCGGCTTGTAGCCCTTCCT 300
QY      301  GTCTTTGGGGCTGCACCTGTGCTGAGAGTGTCAACAGAGAGATGGAAACCACTGGTGGGA 360
Db      301  GTCTTTGGGGCTGCACCTGTGCTGAGAGTGTCAACAGAGAGATGGAAACCACTGGTGGGA 360
QY      361  CAAGTGCAGAGTGGATGTGGCCCTACCTGAGAGACGGGCTGGCTGACTGGATCCACAGC 420
Db      361  CAAGTGCAGAGTGGATGTGGCCCTACCTGAGAGACGGGCTGGCTGACTGGATCCACAGC 420
QY      421  AGTGGGGCTGGCGGAGTTTCACGCTCTATACGGGACGGGGCCCTGGAGAGCGCGGG 480
Db      421  AGTGGGGCTGGCGGAGTTTCACGCTCTATACGGGACGGGGCCCTGGAGAGCGCGGG 480
QY      481  CGTCTCGGGAGGGGAACCTGGGCATCAGTAGGACAGTGTGACGGGGCGGCTGGCACTG 540
Db      481  CGTCTCGGGAGGGGAACCTGGGCATCAGTAGGACAGTGTGACGGGGCGGCTGGCACTG 540
QY      541  GGGGCCCTGGTAACCTGTAGGGGCCCTTTTGTGTAGCAAGTGAA 583
Db      541  GGGGCCCTGGTAACCTGTAGGGGCCCTTTTGTGTAGCAAGTGAA 583

RESULT 5
AX030817  AX030817  583 bp  DNA  linear  PAT 20-SEP-2000
LOCUS      Sequence 6 from Patent WO9735971.
DEFINITION
ACCESSION  AX030817
VERSION     AX030817.1 GI:10278311
KEYWORDS   unidentified
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1
AUTHORS     Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
TITLE       A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
JOURNAL     apoptosis-controlling genes
PATENT: WO 9735971-A 6 02-OCT-1997;
ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU)
; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)
FEATURES
source
1..583
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1..583
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/db_xref="GI:10278312"
/translation="MATEPASADPTALVADFVGYKLRKGVVCGAGPGEPAADFLHQ
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RLREGNWSAVRTVLGVALGALVTVGAFASK"
BASE COUNT  105 a 157 c 210 g 111 t
ORIGIN

Query Match
Best Local Similarity 99.2%; Score 578.2; DB 6; Length 583;
Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  ATGGCCACCCAGCCTCGGCCCCAGACACACGCGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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QY      61  AAGCTGAGGCAGAGGGTTATGTCTGTGAGCTGGCCCCCGGGAGGGCCACAGCTGAC 120
Db      61  AAGCTGAGGCAGAGGGTTATGTCTGTGAGCTGGCCCCCGGGAGGGCCACAGCTGAC 120
QY      121  CGGCTGCACCAAGCCATCGCGGACGCTGGAGATGAGTTGAGACCCCGCTTCGGCGCACC 180
Db      121  CGGCTGCACCAAGCCATCGCGGACGCTGGAGATGAGTTGAGACCCCGCTTCGGCGCACC 180
QY      181  TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCACGACCAACGCTTCACC 240
Db      181  TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCACGACCAACGCTTCACC 240
QY      241  CAGGTCTCCGACGAACCTTTTCAAGGGGCCCCAACTGGGCGGCTTGTAGCCCTTCCT 300
Db      241  CAGGTCTCCGACGAACCTTTTCAAGGGGCCCCAACTGGGCGGCTTGTAGCCCTTCCT 300
QY      301  GTCTTTGGGGCTGCACCTGTGCTGAGAGTGTCAACAGAGAGATGGAAACCACTGGTGGGA 360
Db      301  GTCTTTGGGGCTGCACCTGTGCTGAGAGTGTCAACAGAGAGATGGAAACCACTGGTGGGA 360
QY      361  CAAGTGCAGAGTGGATGTGGCCCTACCTGAGAGACGGGCTGGCTGACTGGATCCACAGC 420
Db      361  CAAGTGCAGAGTGGATGTGGCCCTACCTGAGAGACGGGCTGGCTGACTGGATCCACAGC 420
QY      421  AGTGGGGCTGGCGGAGTTTCACGCTCTATACGGGACGGGGCCCTGGAGAGCGCGGG 480
Db      421  AGTGGGGCTGGCGGAGTTTCACGCTCTATACGGGACGGGGCCCTGGAGAGCGCGGG 480
QY      481  CGTCTCGGGAGGGGAACCTGGGCATCAGTAGGACAGTGTGACGGGGCGGCTGGCACTG 540
Db      481  CGTCTCGGGAGGGGAACCTGGGCATCAGTAGGACAGTGTGACGGGGCGGCTGGCACTG 540
QY      541  GGGGCCCTGGTAACCTGTAGGGGCCCTTTTGTGTAGCAAGTGAA 583
Db      541  GGGGCCCTGGTAACCTGTAGGGGCCCTTTTGTGTAGCAAGTGAA 583

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RESULT 6
BC021198  BC021198  1437 bp  mRNA  linear  PRI 22-JAN-2002
LOCUS      Homo sapiens, BCL2-like 2, clone MGC:10675 IMAGE:3944307, mRNA,
DEFINITION complete cds.
ACCESSION  BC021198
VERSION     BC021198.1 GI:18203706
KEYWORDS   MGC.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Eukarya; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Strausberg,R.
1..(bases 1 to 1437)
Direct Submission
Submitted (14-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-3590,
USA
NHL-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapsb@mail.nih.gov
Tissue Procurement: DCTP/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov

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REMARK
COMMENT

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Zhang, L.-H. and Green, S.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 15 Row: K Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14574571.

FEATURES

Location/Qualifiers
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BASE COUNT

ORIGIN

Query Match 99.2%; Score 578.2; DB 9; Length 1437;
Best Local Similarity 99.5%; Pred. No. 7,5e-120;
Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGGGACCCAGCCCTGGCCCCAGACACACAGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
Db 176 ATGGGACCCAGCCCTGGCCCCAGACACACAGGGCTCTGGTGGCAGACTTTGTAGTTAT 235
QY 61 AAGCTGAGCAGAGGGTTATGTTGTGAGAGTGGCCCCGGGAGGGCCGACGACTGAC 120
Db 236 AAGCTGAGCAGAGGGTTATGTTGTGAGAGTGGCCCCGGGAGGGCCGACGACTGAC 295
QY 121 CGCTGACCAAGCCATCGGGCAGCTGAGATGATTCGACACCGCTTCGGGGCACC 180
Db 296 CCAGTGCACCAAGCCATCGGGCAGCTGAGATGATTCGACACCGCTTCGGGGCACC 355
QY 181 TTCTCTGATCTGGCGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAGCTTCACC 240
Db 356 TTCTCTGATCTGGCGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAGCTTCACC 415
QY 241 CAGGTCTCGACGAACTTTTCAAGGGGCCCCAACTGGGGCCGCTTGTAGCCTTCTTT 300
Db 416 CAGGTCTCGATSAATTTTCAAGGGGCCCCAACTGGGGCCGCTTGTAGCCTTCTTT 475
QY 301 GTCTTTGGGGCTGCACCTGTGCTGAGAGTGTCACAAAGGAGATGGAACCACTGGTGGGA 360
Db 476 GTCTTTGGGGCTGCACCTGTGCTGAGAGTGTCACAAAGGAGATGGAACCACTGGTGGGA 535
QY 361 CAAAGTGACAGAGTGGTGGCTACCTGAGAGACGGCGCTGGCTGACTGGATCCACAGC 420
Db 536 CAAAGTGACAGAGTGGTGGCTACCTGAGAGACGGCGCTGGCTGACTGGATCCACAGC 595
QY 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGGACGGGGCCCTGGAGAGCGCGGG 480
Db 596 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGGACGGGGCCCTGGAGAGCGCGGG 655
QY 481 CGTCTGCGGGAGGGAACCTGGGCATCAGTGAGAGCAGTCTGACGGGGCCCTGGCACTG 540
Db 656 CGTCTGCGGGAGGGAACCTGGGCATCAGTGAGAGCAGTCTGACGGGGCCCTGGCACTG 715
QY 541 GGGGGCCCTGGTAACCTGTAGGGCCCTTTTGTAGCAAGTGAA 583
Db 716 GGGGGCCCTGGTAACCTGTAGGGCCCTTTTGTAGCAAGTGAA 758

RESULT 7

AR020780
LOCUS
DEFINITION
AR020780
ACCESSION
AR020780.1
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Sequence 2 from patent US 5789201.
GI:3975395
Unknown.
Unclassified.
Guastella, J.
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Location/Qualifiers
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/organism="unknown"

BASE COUNT 106 a 154 c 208 g 111 t
ORIGIN

Query Match 98.2%; Score 572.6; DB 6; Length 579;
Best Local Similarity 99.3%; Pred. No. 1.6e-118;
Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGGGACCCAGCCCTGGCCCCAGACACACAGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
Db 1 ATGGGACCCAGCCCTGGCCCCAGACACACAGGGCTCTGGTGGCAGACTTTGTAGTTAT 60

QY 61 AAGCTGAGCAGAGGGTTATGTTGTGAGAGTGGCCCCGGGAGGGCCGACGACTGAC 120
Db 61 AAGCTGAGCAGAGGGTTATGTTGTGAGAGTGGCCCCGGGAGGGCCGACGACTGAC 120

QY 121 CCAGTGCACCAAGCCATCGGGCAGCTGAGATGATTCGACACCGCTTCGGGGCACC 180
Db 121 CCAGTGCACCAAGCCATCGGGCAGCTGAGATGATTCGACACCGCTTCGGGGCACC 180

QY 181 TTCTCTGATCTGGCGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAGCTTCACC 240
Db 181 TTCTCTGATCTGGCGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAGCTTCACC 240

QY 241 CAGGTCTCGACGAACTTTTCAAGGGGCCCCAACTGGGGCCGCTTGTAGCCTTCTTT 300
Db 241 CAGGTCTCGCATGAACCTTTTCAAGGGGCCCCAACTGGGGCCGCTTGTAGCCTTCTTT 300

QY 301 GTCTTTGGGGCTGCACCTGTGCTGAGAGTGTCACAAAGGAGATGGAACCACTGGTGGGA 360
Db 301 GTCTTTGGGGCTGCACCTGTGCTGAGAGTGTCACAAAGGAGATGGAACCACTGGTGGGA 360

QY 361 CAAAGTGACAGAGTGGTGGCTACCTGGAGACGGCGCTGGCTGACTGGATCCACAGC 420
Db 361 CAAAGTGACAGAGTGGTGGCTACCTGGAGACGGCGCTGGCTGACTGGATCCACAGC 420

QY 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGGACGGGGCCCTGGAGAGCGCGGG 480
Db 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGGACGGGGCCCTGGAGAGCGCGGG 480

QY 481 CGTCTGCGGGAGGGAACCTGGGCATCAGTGAGAGCAGTCTGACGGGGCCCTGGCACTG 540
Db 481 CGTCTGCGGGAGGGAACCTGGGCATCAGTGAGAGCAGTCTGACGGGGCCCTGGCACTG 540

QY 541 GGGGGCCCTGGTAACCTGTAGGGCCCTTTTGTAGCAAG 579
Db 541 GGGGGCCCTGGTAACCTGTAGGGCCCTTTTGTAGCAAG 579

RESULT 8

AF096291
LOCUS
DEFINITION
AF096291
ACCESSION
AF096291.1
VERSION

582 bp mRNA linear
Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.

KEYWORDS

SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 582)
 Hamner, S., Skoglosa, Y. and Lindholm, D.
 Differential expression of bcl-w and bcl-x messenger RNA in the
 developing and adult rat nervous system
 Neuroscience 91 (2), 673-684 (1999)

JOURNAL 99292146
 MEDLINE 10366024
 PUBMED

REFERENCE 2 (bases 1 to 582)
 Hamner, S., Skoglosa, Y. and Lindholm, D.
 Direct Submision

TITLE Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala
 JOURNAL University, Box 587, BMC, Uppsala 751 23, Sweden
 Location/Qualifiers

FEATURES

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 111 a 157 c 200 g 114 t

gene

CDS

BASE COUNT 111 a 157 c 200 g 114 t
 ORIGIN

Query Match 91.3%; Score 532.4; DB 10; Length 582;
 Best Local Similarity 94.7%; Pred. No. 1.7e-139;
 Matches 55; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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QY 61 AAGCTGAGGCGAAGAGTTTATCTGTGGAGTGTGCGCCCGGGAGGCGCCAGAGCTGAC 120
 DB 61 AAGCTGAGGCGAAGAGTTTATCTGTGGAGTGTGCGCCCGGGAGGCGCCAGAGCTGAC 120

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QY 181 TTCTCTGATCTGGCGGCTCAGCTGTCATGTGACCCAGGCTCAGCCAGCAACGCTTACC 240
 DB 181 TTCTCTGATCTGGCGGCTCAGCTGTCATGTGACCCAGGCTCAGCCAGCAACGCTTACC 240

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QY 541 GGGGGCCCTGGTAACTCTAGGGGCTTTTTCGTAGCAAGTGA 582
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RESULT 9

LOCUS AR020779 579 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 1 from patent US 5789201.
 ACCESSION AR020779
 VERSION AR020779.1 GI:3975394
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 579)
 Guastella, J.

TITLE Genes coding for bcl-y a bcl-2 homologue
 JOURNAL Patent: US 5789201-A 1 04-AUG-1998;
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Query Match 90.5%; Score 527.8; DB 6;
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QY 1 ATGGGACCCCGAGCTCGGCCACAGACACACGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
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Best Local Similarity 94.2%; Pred. No. 1.6e-108;
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QY 61 AAGCTGAGGACGAAGGTTATCTGTGTGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 120
DB |||||||
239 AAGCTGAGGACGAAGGTTATCTGTGTGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 298
QY 121 CGCTGACACCAAGCATCGGCGACGTGGAGATGAGTTGAGAGCCGCTTCGGCGCAC 180
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DB |||||||
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DB |||||||
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RESULT 12
AY170344 3473 bp mRNA linear RCD 04-JAN-2003
LOCUS Mus musculus Bcl2-like protein 2 mRNA, complete cds.
DEFINITION AY170344
ACCESSION AY170344
VERSION AY170344.1 GI:27497698
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3473)
AUTHORS Su, H.-Y.
TITLE Extraction from neonatal mouse skin after IGF-1 stimulation

Unpublished
REFERENCE 2 (bases 1 to 3473)
AUTHORS Su, H.-Y.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2002) Biotechnology, Pingtung University, No. 1,
Hsueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan
FEATURES
Location/Qualifiers
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Query Match 88.6%; Score 516.4; DB 10; Length 3473;
Best Local Similarity 93.0%; Pred. No. 5.3e-106;
Matches 541; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
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176 ATGGCAACCCAGCTCAACCCAGACACACGGGCTCTAGTGGCTTACTTTGTAGGCTAT 235
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DB |||||||
236 CAGCTGAGGACGAAGGTTATGTCTGTGAGCTGGCCCTGGGAAAGGGCCAGCCCGCAC 295
QY 121 CGCTGCAACCAAGCATCGGCGACGTGGAGATGAGTTGAGACCCGCTTCGGCGCAC 180
DB |||||||
296 CGCTGCAACCAAGCATCGGCGCTGTGAGAGAGATGAGACCCGCTTCGGCGCAC 355
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DB |||||||
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RESULT 13
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LOCUS AX022531 581 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 8 from Patent EP0932674.
ACCESSION AX022531
VERSION AX022531.1 GI:10046127
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.
AUTHORS A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
TITLE apoptosis-controlling genes
JOURNAL Patent: EP 0932674-A 8 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
FEATURES
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BASE COUNT 205 a 164 c 195 g 117 t
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Best Local Similarity 91.9%; Pred. No. 1.7e-103;
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
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DEFINITION Sequence 8 from Patent WO9735971.
ACCESSION AX030819
VERSION AX030819.1 GI:10278313
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.
AUTHORS A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
TITLE apoptosis-controlling genes
JOURNAL Patent: WO 9735971-A 8 02-OCT-1997;
ADAMS JERRY MCKEE (AU); HOLMGREN SHAUN P (AU); CORY SUZANNE (AU);
GIBSON LEONIE M (AU); AMRAD OPERATIONS PTY LTD (AU)
FEATURES
Location/Qualifiers
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RLREGNWA"
BASE COUNT 105 a 164 c 195 g 117 t
ORIGIN
Query Match 86.8%; Score 505.8; DB 6; Length 581;
Best Local Similarity 91.9%; Pred. No. 1.7e-103;
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 1 ATGGGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
DB 1 ATGGGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGTGAATTTGTAGGTTAT 60
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QY      541  GGGGCGCCCTGGTAACCTGTAGGGGCGCTTTTGTGTAGCAAGTG 581
DB      541  GGGGCGCCCTGGTAACCTGTAGGGGCGCTTTTGTGTAGCAAGTG 581

RESULT 15
AC128940
LOCUS   AC128940
DEFINITION
Rattus norvegicus clone CH230-43402, *** SEQUENCING IN PROGRESS
AC128940
VERSION AC128940.3 GI:25073546
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
SOURCE   Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 220818)
Muzny,D,Marie., Metzker,M, Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alebrooks,S., Amin,A., Anquiano,D.,
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Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
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Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
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Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
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Fernandez,S., Firley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,M., Guevara,W.,
Gunaratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hoques,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,S., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jollivet,A.,
Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Lit,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A.,
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Popper,P., Poidexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Snajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Taber,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmali,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wlezyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,

```

```

TITLE
JOURNAL
REFERENCE
2 (bases 1 to 220818)
Worley,K.C.
Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 220818)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23269386.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KBEM
Center clone name: CH230-43402
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 202395 bases at least Q40
Consensus quality: 205627 bases at least Q30
Consensus quality: 207823 bases at least Q20
Estimated insert size: 212631; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 174472: contig of 174472 bp in length
* 174473 174572: gap of unknown length
* 174573 218266: contig of 43694 bp in length
* 218267 218366: gap of unknown length
* 218367 219597: contig of 1231 bp in length
* 219598 219697: gap of unknown length
* 219698 220818: contig of 1121 bp in length.
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/note="wgs_contig"
BASE COUNT 62390 a 42027 c 41606 g 62941 t 11854 others
ORIGIN
Query Match 76.5% Score 446; DB 2; Length 220818;

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Best Local Similarity 87.1%; Pred. No. 2.1e-90;
Matches 507; Conservative 0; Mismatches 60; Indels 15; Gaps 1;

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Db	142046	AAGCTGAGGTGAAGGGTTATGCTGTGGAGTGGCCCTGGAAAGGGCCAGCAGCTGAT	142105
QY	121	CCGCTGCACCAAGCCATGGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGCGCACC	180
Db	142106	CTGCTACACCAAGCCATGCATGCTCTGGAGCAGATTTGAGACCCGCTTCGGGTACACC	142165
QY	181	TTCTCTGATCTCGGGCTCAGCTGATGTGACCCAGSCTCAGCCAGCAACGCTTCACC	240
Db	142166	TTCTCTGACCTAGCCACTCAGCAACATGTGACCCAGSCTCAGCCAGCAACGCTTCACC	142225
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Db	142226	CAGGTTTCGATGAACCTTTTCAAGGGGGCCCACTGGGGACGCTCTTGGCATTCCT	142285
QY	301	GTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGCA	360
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QY	361	CAAGTGCAGGAGTGGATGGTGCCTACCTGGAGACGGGCTGGCTGATGATCCACAGC	420
Db	142346	CAAGTGCAGGACTGGATGGTGGCTACCTGGAGACATGCTGACTGACTGGATCGACAGC	142405
QY	421	AGTGGGGCTGGCGGAGTTACAGCTCTATACGGGACGGGGCCCTGAGGAGCGCGGG	480
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QY	541	GGGGCCCTGGTAACCTGTAGGGCCCTTTTGTAGCAAGTGA	582
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Search completed: October 27, 2003, 13:01:24
Job time : 1741.99 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:02:30 ; Search time 177.152 Seconds
(without alignments)
8883.744 Million cell updates/sec

Title: US-C9-925-674A-6

Perfect score: 583

Sequence: 1 atggcgaccacgctcggc.....ctttttgctagcaagt-gaa 583

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5:05512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 19Jun03:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582	99.8	582	24	Human bcl-w polynuc
2	582	99.8	582	24	Human bcl-w DNA fr
3	582	99.8	582	24	Human bcl-w DNA SE
4	582	99.8	582	24	Human polynucleoti
5	579.8	99.5	3542	25	Human bcl-2 gene S
6	578.2	99.2	583	18	Human bcl-w DNA.
7	578.2	99.2	583	20	Human bcl-w gene d
8	577.8	99.1	581	20	Human bcl-w gene.

9	572.6	98.2	579	19	AAV28334	Human bcl-y gene.
10	572.6	98.2	579	20	AAV15946	cDNA encoding the
11	527.8	90.5	579	19	AAV28333	Rat bcl-y gene. R
12	527.8	90.5	579	20	AAV15945	cDNA encoding the
13	526.6	90.3	581	20	AAV25133	Mouse bcl-w gene.
14	505.8	86.8	581	18	AAV96578	Mouse bcl-w DNA.
15	505.8	86.8	581	20	AAV25135	Mouse bcl-w gene d
16	428.8	73.6	1098	19	AAV41925	Nucleotide sequenc
17	428.4	73.5	1864	19	AAV59630	Human secreted pro
18	428.4	73.5	1864	24	ABV73617	Human cDNA #1 for
19	257	44.1	6049	24	ABV73617	Human immune syste
20	223	38.3	6049	24	ABV73617	Human breast cell
21	150	25.7	150	22	ABA47382	Human foetal liver
22	150	25.7	150	22	ABA65269	Probe #10336 for g
23	150	25.7	150	22	ABA32370	Human brain expres
24	150	25.7	150	22	AAK13683	Human bone marrow
25	150	25.7	150	22	AAK39424	Probe #10169 for g
26	150	25.7	150	22	AAI20236	Probe #14124 used
27	150	25.7	150	22	AAI45438	Probe #5931 used t
28	150	25.7	150	22	AAI05940	Human liver single
29	150	25.7	150	23	ABS39016	Human genome-deriv
30	150	25.7	150	24	ABS13513	Rat wild-type Bcl-
31	143	24.5	1742	22	AAF75960	Phase-1 Rat CT gen
32	133.8	23.0	695	24	ABT09346	Mutant bcl-XL cod
33	131	22.5	636	22	AAH48169	cDNA clone HP03584
34	131	22.5	702	22	AAH43464	Human thymus BCL-X
35	131	22.5	926	16	AAQ81698	Bcl-XL gene. Homo
36	131	22.5	926	17	AAQ40079	Bcl-x gene. Homo
37	131	22.5	926	21	AAZ93614	Human bcl-x cDNA.
38	131	22.5	926	22	AAZ93614	Human bcl-XL nucle
39	131	22.5	926	22	AAZ93614	Human cDNA differe
40	131	22.5	926	25	ABT16641	Human bcl-2 gene S
41	131	22.5	926	25	ABT16641	Bcl-XL-DTR apoptos
42	131	22.5	1236	22	AAZ00247	Base sequence of t
43	131	22.5	7372	20	AAZ33182	Phase-1 Rat CT gen
44	128.6	22.1	660	24	ABT09345	DNA encoding human
45	128.2	22.0	720	22	AAH45295	

ALIGNMENTS

RESULT 1

ABZ35729
ID ABZ35729 standard; DNA; 582 BP.

XX AC ABZ35729;

XX AC ABZ35729;

DC 07-FEB-2003 (first entry)

XX Human bcl-w polynucleotide SEQ ID NO 37.

DE Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;
XX protozoacide; gene expression; antisense; tumour; infection; Plasmodium;
XX virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
XX Hepatitis C virus; human papilloma virus; gene; ds.

XX Homo sapiens.

XX DE10100588-AL.

XX 18-JUL-2002.

XX 09-JAN-2001; 2001DE-1000588.

XX 09-JAN-2001; 2001DE-1000588.

XX (R30-) RIBOPHARMA AG.

XX Kreutzer R, Limmer S, Rost S, Hadwiger P;

XX WP; 2002-683450/74.

PT Inhibiting expression of target genes, useful e.g. for treating tumors,
PT by introducing into cells two double-stranded RNAs that are
PT complementary to the target -
XX
XX
PS Claim 13; Page 30-31; 100pp; German.
XX
CC The invention relates to inhibiting expression of a target gene in a cell
CC by introducing at least two oligoribonucleotides (dsRNAi and II), both
CC with a double-stranded (ds) structure of at most 49 sequential nucleotide
CC pairs. At least part of one strand (S₁, S₂) of the ds structures in each
CC of dsRNAi and II are complementary to regions in the target gene. The
CC method uses antisense inhibition of gene expression using double stranded
CC RNA inhibition (RNAi). The method is particularly used to treat tumours
CC or infections, especially by Plasmodium or viruses/viroids (pathogenic on
CC humans, animals or plants). The method provides more effective inhibition
CC of expression than known methods using a single dsRNA, even at very low
CC concentrations. When dsRNA has at least one unpaired nucleotide at the
CC end, stability (and thus effective concentration in the cell) is
CC improved and efficiency can be increased further by pretreating the cells
CC with interferon. The present sequence is that of a target DNA of the
CC invention.
XX
XX
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 other;

Query Match 99.8%; Score 582; DB 24; Length 582;
Best Local Similarity 100.0%; Pred. No. 3.7e-135;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGACCCAGCCTCGGCCCCAGACACACACGGGCTCTGGTGGACAGCTTTGTAGGTTAT 60
DB 1 ATGGGACCCAGCCTCGGCCCCAGACACACACGGGCTCTGGTGGACAGCTTTGTAGGTTAT 60
QY 61 AAGCTGAGCAGAAAGGTTATCTGTGAGCTGCGCCCGGGAGGGCCAGCAGCTTAC 120
DB 61 AAGCTGAGCAGAAAGGTTATCTGTGAGCTGCGCCCGGGAGGGCCAGCAGCTTAC 120
QY 121 CGCTGTGACACAGCAGTGGGACCTGGAGATGAGTTCGAGACCGGCTTCGGGGCACC 180
DB 121 CGCTGTGACACAGCAGTGGGACCTGGAGATGAGTTCGAGACCGGCTTCGGGGCACC 180
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCTGATGACCCAGGCTCAGCCAGCAGACGCTTCACC 240
DB 181 TTCTCTGATCTGGCGGCTCAGCTGCTGATGACCCAGGCTCAGCCAGCAGACGCTTCACC 240
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DB 241 CAGGTCTCCGACGAACCTTTTCAAGGGGCGCCCAACTGGGGCGGCTTGTAGCCTTCTTT 300
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DB 301 GTCTTTGGGGTGCACCTGTGCTGAGAGTGTCAACAGGAGATGGAACCTGGTGGGA 360
QY 361 CAAAGTGCAGAGTGGATGGTGGCTTACCTGGAGACGGGCTGGCTGACTGGATCCACAGC 420
DB 361 CAAAGTGCAGAGTGGATGGTGGCTTACCTGGAGACGGGCTGGCTGACTGGATCCACAGC 420
QY 421 AGTGGGGGCTGGGCGAGTTCACAGCTCTATACGGGACGGGGCCCTGAGAGAGCGCGG 480
DB 421 AGTGGGGGCTGGGCGAGTTCACAGCTCTATACGGGACGGGGCCCTGAGAGAGCGCGG 480
QY 481 CGTCTCGGGAGGGGAACCTGGGACATCAGTGAGGACAGTCTCAGCGGGGSCCTGGCACTG 540
DB 481 CGTCTCGGGAGGGGAACCTGGGACATCAGTGAGGACAGTCTCAGCGGGGSCCTGGCACTG 540
QY 541 GGGGGCCCTGGTAACCTAGGGGCTTTTGTAGCAAGTGA 582
DB 541 GGGGGCCCTGGTAACCTAGGGGCTTTTGTAGCAAGTGA 582

RESULT 2
ABX09972
ID ABX09972 standard; DNA; 582 BP.
XX

AC ABX09972;
XX
XX 23-JAN-2003 (first entry;
XX
DE Human bcl-w DNA fragment SEQ ID 37.
XX
XX Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;
XX prion; inhibition; human; ds.
XX
XX Homo sapiens.
XX
XX DE:0100587-Cl.
XX
XX 23-NOV-2002.
XX
XX 09-JAN-2001; 2001DE-1000587.
XX
XX 09-JAN-2001; 2001DE-1000587.
XX
XX (RIBO-) RIBOPHARMA AG.
XX
XX Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
XX WPI; 2002-742209/81.
XX
XX Inhibiting expression of target genes, e.g. oncogenes, in cells, by
XX introduction of complementary double-stranded oligoribonucleotide,
XX after treating the cell with interferon -
XX
XX Disclosure; Page 35-36; 98pp; German.
XX
XX This invention describes a novel method for inhibiting expression of a
XX target gene by introducing into the cell that contains the target gene
XX at least one oligoribonucleotide (dsRNAi) that has a double-stranded
XX (ds) structure of not more than 49 consecutive nucleotides (nt), where
XX at least a segment of one strand of the ds structure is complementary
XX with the target gene and the cells are treated with interferon before
XX introduction of dsRNAi. The method is used to inhibit expression of
XX target genes, particularly oncogenes, cytokine genes, Id (not defined)
XX protein genes, developmental or prion genes, or genes expressed in
XX pathogenic organisms (particularly plasmidia) or in viruses or viroids
XX (pathogenic in humans, animals or plants). Treating the cells with
XX interferon greatly increases the extent to which dsRNA can inhibit
XX expression of the target genes, and the effect is even greater when dsRNA
XX are modified to increase their stability. ABX09936-ABX10075 represent
XX gene fragments used to illustrate the method of the invention.
XX
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 other;

Query Match 99.8%; Score 582; DB 24; Length 582;
Best Local Similarity 100.0%; Pred. No. 3.7e-135;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGACAGCTTTGTAGGTTAT 60
DB 1 ATGGGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGACAGCTTTGTAGGTTAT 60
QY 61 AAGCTGAGCAGAAAGGTTATGCTGTGAGCTGCGCCCGGGAGGGCCAGCAGCTTAC 120
DB 61 AAGCTGAGCAGAAAGGTTATGCTGTGAGCTGCGCCCGGGAGGGCCAGCAGCTTAC 120
QY 121 CGCTGTGACACAGCAGTGGGGACCTGGAGATGAGTTCGAGACCGGCTTCGGGGCACC 180
DB 121 CGCTGTGACACAGCAGTGGGGACCTGGAGATGAGTTCGAGACCGGCTTCGGGGCACC 180
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCTGATGACCCAGGCTCAGCCAGCAGACGCTTCACC 240
DB 181 TTCTCTGATCTGGCGGCTCAGCTGCTGATGACCCAGGCTCAGCCAGCAGACGCTTCACC 240
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGCGCCCAACTGGGGCGGCTTGTAGCCTTCTTT 300
DB 241 CAGGTCTCCGACGAACCTTTTCAAGGGGCGCCCAACTGGGGCGGCTTGTAGCCTTCTTT 300

QY 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTCTCAACAGGAGATGGACCACTGGTGGGA 360
DB 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTCTCAACAGGAGATGGACCACTGGTGGGA 360
QY 361 CAAGTGACAGGAGTGGATGGTGGCTTACCTGGAGACGGGGCTGGCTGACTGGATCCACAGC 420
DB 361 CAAGTGACAGGAGTGGATGGTGGCTTACCTGGAGACGGGGCTGGCTGACTGGATCCACAGC 420
QY 421 AGTGGGGCTGGGGGAGATTACAGCTCTATACGGGAGACGGGGCCCTGGAGAGGCGCGG 480
DB 421 AGTGGGGCTGGGGGAGATTACAGCTCTATACGGGAGACGGGGCCCTGGAGAGGCGCGG 480
QY 481 CGTCTGCGGAGGGGAACCTGGGCATCAGTGAGGACAGTGCCTGACGGGGCGGTGSCACTG 540
DB 481 CGTCTGCGGAGGGGAACCTGGGCATCAGTGAGGACAGTGCCTGACGGGGCGGTGSCACTG 540
QY 541 GGGGCCCTGGTAACCTGTAGGGGCCCTTTTTCCTAGCAAGTGA 582
DB 541 GGGGCCCTGGTAACCTGTAGGGGCCCTTTTTCCTAGCAAGTGA 582
RESULT 3
ABV78153
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XX AC ABV78153;
XX XX
XX DT 15-NOV-2002 (first entry)
XX XX
XX DE Human bcl-w DNA SEQ ID NO 37.
XX XX
XX KW RNA inhibition; dsRNAi; gene expression inhibitor; oncogene; cytostatic;
XX KW virucide; protozoacide; gene; ds.
XX OS Homo sapiens.
XX PN WO200255693-A2.
XX XX
XX PD 18-JUL-2002.
XX XX
XX PF 09-JAN-2002; 2002WO-EP00152.
XX PR 09-JAN-2001; 2001DE-1000586.
XX PR 26-OCT-2001; 2001DE-1055280.
XX PR 29-NOV-2001; 2001DE-1058411.
XX PR 07-DEC-2001; 2001DE-1060151.
XX PA (RIBO-) RIBOPHARMA AG.
XX XX
XX PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX DR WPI; 2002-590671/63.
XX XX
XX PT Inhibiting expression of target gene, useful e.g. for inhibiting
XX PT oncogenes, by administering double-stranded RNA complementary to the
XX PT target and having an overhang -
XX XX
XX PS Claim 10; Page 134; 203pp; German.
XX XX
XX CC The invention relates to inhibiting expression of a target gene (I) in a
XX CC cell by introducing an inhibitory RNA (dsRNAi) having a double-stranded
XX CC structure of at most 49 consecutive bases. At least part of one strand
XX CC (asi) of dsRNAi is complementary to (I) and at least one end of dsRNAi
XX CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
XX CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
XX CC in humans, also genes in Plasmodium or in viruses or viroids that are
XX CC pathogenic for humans, animals or plants. Introducing an overhang into
XX CC dsRNA greatly increases effectiveness for inhibiting gene expression,
XX CC both in vivo and in vitro and also increases stability and thus the
XX CC effective concentration inside the cell. The present sequence is that of
XX CC a gene related to the invention.
XX XX
XX SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 other;

Query Match 99.8%; Score 582; DB 24; Length 582;
Best Local Similarity 100.0%; Pred. No. 3.7e-135;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCCACCCAGACCTCGGCCCCAGACACACAGGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
DB 1 ATGGCCACCCAGACCTCGGCCCCAGACACACAGGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
QY 61 AAGCTGAGGACGAAGGGTTATGTCTGTGAGCTGGCCCCCGGGGAGGGCCACAGCTGAC 120
DB 61 AAGCTGAGGACGAAGGGTTATGTCTGTGAGCTGGCCCCCGGGGAGGGCCACAGCTGAC 120
QY 121 CGCTCGACCAAGCCATCGGGCAGCTGGAGATGAGTTGAGACCCGCTTCGGGGCCGACC 180
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QY 361 CAAGTGACAGGATGGATGGTGGCTTACCTGGAGACGGGGCTGCTGACTGGATCCACAGC 420
DB 361 CAAGTGACAGGATGGATGGTGGCTTACCTGGAGACGGGGCTGCTGACTGGATCCACAGC 420
QY 421 AGTGGGGCTGGGGGAGTTTACAGCTCTATACGGGAGACGGGGCCCTGGAGGAGGCGCGG 480
DB 421 AGTGGGGCTGGGGGAGTTTACAGCTCTATACGGGAGACGGGGCCCTGGAGGAGGCGCGG 480
QY 481 CGTCTCGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCGCTGGCACTG 540
DB 481 CGTCTCGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCGCTGGCACTG 540
QY 541 GGGGCCCTGGTAACCTGTAGGGGCCCTTTTTCCTAGCAAGTGA 582
DB 541 GGGGCCCTGGTAACCTGTAGGGGCCCTTTTTCCTAGCAAGTGA 582
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TJ ABL91694 standard; DNA; 582 BP.
XX AC ABL91694;
XX XX
XX DT 28-MAY-2002 (first entry)
XX XX
XX DE Human polynucleotide SEQ ID NO 37.
XX XX
XX KW Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
XX KW Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
XX KW cytostatic; virucide; protozoacide; antibacterial; ds.
XX OS Homo sapiens.
XX XX
XX PN DE10100586-Cl.
XX XX
XX PD 11-APR-2002.
XX XX
XX PF 09-JAN-2001; 2001DE-1000586.
XX XX
XX PR 09-JAN-2001; 2001DE-1000586.
XX XX
XX PA (RIBO-) RIBOPHARMA AG.
XX XX
XX PI Kreutzer R, Limmer S, Rost S, Hadwiger P;

```
XX DR WPI; 2002-270454/32.
XX AC
XX XX Inhibiting gene expression in cells, useful for e.g. treating tumors,
PT by introducing double-stranded complementary oligoRNA having unpaired
PT terminal bases
XX PS
XX PS Claim 13; Page 32; 104pp; German.
XX XX The invention relates to a method for inhibiting expression of a target
CC gene (ABL91656-ABL91797) in a cell by introducing at least one
CC oligoribonucleotide that has a double-stranded structure consisting of at
CC most 49 sequential nucleotide pairs, with at least part of one strand
CC complementary with the target gene and has at least one end a
CC single-stranded segment of 1-4 nt. The method provides
CC oligoribonucleotides for antisense inhibition of gene expression useful
CC e.g. for treating tumors but the oligoribonucleotides may also be
CC directed against genes present in pathogens (e.g. Plasmodium or
CC viruses/viroids, pathogenic or humans, animals or plants) or against
CC cytokine, id, developmental or prion genes. The method provides more
CC effective inhibition of gene expression than use of known
CC oligonucleotides, probably because the unpaired overhang increases
CC stability and thus intracellular concentration.
XX PS
XX PS Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 other;
XX DR
XX DR Query Match 99.8%; Score 582; DB 24; Length 582;
XX XX Best Local Similarity 100.0%; Pred. No. 3.7e-135;
XX XX Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGACCCAGCCTCGCCCCACACACACACACACCGGCTCTGGTGGCAGACTTTGTAGTTAT 60
DB 1 ATGGGACCCAGCCTCGCCCCACACACACACACACCGGCTCTGGTGGCAGACTTTGTAGTTAT 60
QY 61 AAGCTGAGCAGAAAGGTTATCTGTGAGCTGGCCCGGGAGGGCCAGACCTGAC 120
DB 61 AAGCTGAGCAGAAAGGTTATCTGTGAGCTGGCCCGGGAGGGCCAGACCTGAC 120
QY 121 CGGCTGCACCAAGCATGCGGCAGCTGAGATGATGAGACCCGCTTCGGGGCACC 180
DB 121 CGGCTGCACCAAGCATGCGGCAGCTGAGATGATGAGACCCGCTTCGGGGCACC 180
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGGCTTAC 240
DB 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGGCTTAC 240
QY 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCGGCTGTAGCCTTCTT 300
DB 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCGGCTGTAGCCTTCTT 300
QY 301 GTCTTTGGGGCTGCACTGTGTCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360
DB 301 GTCTTTGGGGCTGCACTGTGTCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360
QY 361 CAAGTGCAGAGTGTGATGTGGCTTACCTGAGAGCGCGCTGGCTGATCCACAGC 420
DB 361 CAAGTGCAGAGTGTGATGTGGCTTACCTGAGAGCGCGCTGGCTGATCCACAGC 420
QY 421 AGTGGGGGCTGGCGGAGTTTACAGCTCTATACGGGGAGCGGGCCCTGAGGAGCGCGG 480
DB 421 AGTGGGGGCTGGCGGAGTTTACAGCTCTATACGGGGAGCGGGCCCTGAGGAGCGCGG 480
QY 481 CGTCTCGGGAGGGGAACCTGGGATCAGTGAGAGCAGTCTCAGCGGGGCCCTGGCAGCTG 540
DB 481 CGTCTCGGGAGGGGAACCTGGGATCAGTGAGAGCAGTCTCAGCGGGGCCCTGGCAGCTG 540
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTAGCAAGTGA 582
DB 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTAGCAAGTGA 582
RESULT 5
ABT16642
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ID ABT16642 standard; DNA; 3542 BP.
XX AC
XX AC ABT16642;
XX XX 03-APR-2003 (first entry)
XX XX Human bcl-2 gene SEQ ID No 4.
XX XX
XX KW Anti-tumour; DNzyme; bcl-2 gene; tumour; malignant; chemotherapy;
XX KW radiation therapy; catalytic domain; enzyme; human; ds.
XX OS Homo sapiens.
XX XX MO200299090-A1.
XX FD 12-DEC-2002.
XX PF 07-JUN-2002; 2002WO-AJ00739.
XX XX 07-JUN-2001; 2001AU-0005527.
XX XX (JOHN J) JOHNSON & JOHNSON RES PTY LTD.
XX XX Sun J. Wang L, Turner RJ, Saravolac EG, Dass CR;
XX XX WPI; 2003-140617/13.
XX XX Novel DNzyme useful for treating tumors, and for enhancing the
XX PT sensitivity of malignant or virus infected cells to therapy, comprises
XX PT a catalytic domain and binding domain contiguous to the catalytic
XX PT domain -
XX PS
XX PS Disclosure; Page 44-45; 67pp; English.
XX CC The invention relates to a DNzyme which specifically cleaves mRNA
XX CC transcribed from a member of the bcl-2 gene family. The DNzymes comprise
XX CC a catalytic domain, binding domains contiguous with the 5' and 3' end of
XX CC the catalytic domain, and therefore hybridise with, the two regions
XX CC immediately flanking the purine residue of the cleavage site within the
XX CC bcl-2 gene family mRNA, at which DNzyme-catalysed cleavage is desired. A
XX CC pharmaceutical composition comprising a DNzyme of the invention is
XX CC useful for treating tumors in a subject, and for enhancing the
XX CC sensitivity of malignant or virus infected cells infected cells to
XX CC therapy. The DNzymes are useful in diagnostics, therapeutics,
XX CC prophylaxis, research agents and in kits. The DNzymes are also
XX CC useful for increasing the susceptibility of tumour cells to anti-tumour
XX CC therapies such as chemotherapy and radiation therapy. This polynucleotide
XX CC sequence represents a human bcl-2 gene of the invention.
XX XX
XX XX Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 other;
XX XX
XX XX Query Match 99.5%; Score 579.8; DB 25; Length 3542;
XX XX Best Local Similarity 99.7%; Pred. No. 2e-134;
XX XX Matches 581; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACACCGGCTCTGGTGGCAGACTTTGTAGTTAT 60
DB 177 ATGGCGACCCAGCCTCGGCCCCAGACACACACCGGCTCTGGTGGCAGACTTTGTAGTTAT 236
QY 61 AAGCTGAGGCGAGAAAGGCTTATGTCTGTGAGCTGGCCCGGGAGGGCCAGACGCTGAC 120
DB 237 AAGCTGAGGCGAGAAAGGCTTATGTCTGTGAGCTGGCCCGGGAGGGCCAGACGCTGAC 296
QY 121 CGGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCCAGACCCGCTTCCGGCGCACC 180
DB 297 CGGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCCAGACCCGCTTCCGGCGCACC 356
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGGCTTAC 240
DB 357 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACACGCTTACC 416
QY 241 CAGGCTCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCGGCTGTAGCCTTCTT 300
```

Db 417 CAGGCTCCGATGAACCTTTTCAAGGGGGCCCCAACTGGGGGGCGCTTGTAGCCTCTT 476
QY 301 GTCTTTGGGGCTGCACGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGTGGGA 360
Db 477 GTCTTTGGGGCTGCACGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGTGGGA 536
QY 361 CAAAGTCAGAGTGGATGGTGGCTTACAGCTCTATACGGGGACGGGGCGCTTGGATCCACAGC 420
Db 537 CAAAGTCAGAGTGGATGGTGGCTTACCTTGGAGACGGGGCTGGCTGACCTGGATCCACAGC 596
QY 421 AGTGGGGCTGGGGGAGTTCACAGCTCTATACGGGGACGGGGCGCTTGGAGAGCGCGG 480
Db 597 AGTGGGGCTGGGGGAGTTCACAGCTCTATACGGGGACGGGGCGCTTGGAGAGCGCGG 656
QY 481 CGTCTCGGGAGGGGAACCTGGGATCAGTGAGGACAGTCTGACGGGGCGCTTGGAGAGCG 540
Db 657 CGTCTCGGGAGGGGAACCTGGGATCAGTGAGGACAGTCTGACGGGGCGCTTGGAGAGCG 716
QY 541 GGGGGCTGGTAACTCTAGGGGCTTTTGTAGCAAGTGAA 583
Db 717 GGGGGCTGGTAACTCTAGGGGCTTTTGTAGCAAGTGAA 759

RESULT 6

AAT96577

ID AAT96577 standard; DNA; 583 BP.

XX AC AAT96577;

XX XX

XX 22-APR-1998 (first entry)

XX Human bcl-w DNA.

XX XX

KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease; ss.

XX OS Homo sapiens.

XX XX

FH Key Location/Qualifiers
FT CDS 1..582 /*tag= a

FT /product= bcl-w

XX XX

XX W09735971-A1.

XX XX

XX 02-OCT-1997.

XX XX

XX 27-MAR-1997; 97MO-AU00199.

XX XX

XX 27-MAR-1996; 96AU-0008965.

XX XX

XX (AMRA-) AYRAD OPERATIONS PTY LTD.

XX PA

XX Adams JM, Cory S, Gibson LM, Holmgren SP;

XX PI

XX WPI: 1997-489635/45.

XX DR P-PSDB; AAW36047.

XX DR

XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT or inhibit cell survival, e.g. for treatment of cancer and
PT degenerative diseases

XX PS

XX Claim 3; Page 48; 86pp; English.

XX XX

CC This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
CC family, extracted from an adult brain library. This gene promotes cell
CC survival, so its modulation is useful in treatment of cancer or
CC auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's
CC disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia,
CC human immunodeficiency virus infection or in cell transplants.
CC Up-regulation of the gene can also be used to modify cell lines cultured
CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
CC and to increase survival of primary explants during genetic modification.

CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
CC antibody production or screening of potential modulators.

XX Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;

XX Query Match 99.2%; Score 578.2; DB 18; Length 583;
XX Best Local Similarity 99.5%; Pred. No. 3.3e-134; Indels 0; Gaps 0;
XX Matches 580; Conservative 0; Mismatches 3;

QY 1 ATGCGACCCAGCCTCGGCCCCAGACACACCGGGCTCTGTGGCAGACTTTGTAGGTTAT 60

Db 1 ATGCGACCCAGCCTCGGCCCCAGACACACCGGGCTCTGTGGCAGACTTTGTAGGTTAT 60

QY 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTTGGCCCCCGGAGAGGCCCCAGCAGCTGAC 120

Db 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTTGGCCCCCGGAGAGGCCCCAGCAGCTGAC 120

QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Db 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

QY 181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240

Db 181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240

QY 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCGCCCTTGTAGCCTTCTTT 300

Db 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCGCCCTTGTAGCCTTCTTT 300

QY 301 GTCTTTGGGGCTGCACCTGTGTGTGAGATGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Db 301 GTCTTTGGGGCTGCACCTGTGTGTGAGATGTCAACAAGGAGATGGAACCACTGGTGGGA 360

QY 361 CAACTGAGGAGTGGATGGTGGCTTACCTGAGACCGCGCTGCTGACTGGATCCACAGC 420

Db 361 CAACTGAGGAGTGGATGGTGGCTTACCTGAGACCGCGCTGCTGACTGGATCCACAGC 420

QY 421 AGTGGGGCTGGGGGAGTTTACAGCTCTATACGGGACCGGGGCCCTGGAGAGGGCGCG 480

Db 421 AGTGGGGCTGGGGGAGTTTACAGCTCTATACGGGACCGGGGCCCTGGAGAGGGCGCG 480

QY 481 CGTCTCGGAGGGGAACTGGGGATCAGTGAGACAGTCTGACGGGGCGCTGGCACTG 540

Db 481 CGTCTCGGAGGGGAACTGGGGATCAGTGAGACAGTCTGACGGGGCGCTGGCACTG 540

QY 541 GGGGCCCTGGTAAGTGTAGGGGCTTTTGTAGCAAGTGAA 583

Db 541 GGGGCCCTGGTAAGTGTAGGGGCTTTTGTAGCAAGTGAA 583

RESULT 7

AA25134

ID AA25134 standard; DNA; 583 BP.

XX AC AA25134;

XX XX

XX 05-JUL-1999 (first entry)

XX Human bcl-w gene derivative.

XX DE

XX Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;

XX KW animal model; ss.

XX OS Homo sapiens.

XX XX

XX WO9913710-A1.

XX PD 25-MAR-1999.

XX XX

XX 16-SEP-1998; 98WO-AU00764.

XX XX

XX 16-SEP-1997; 97AU-0009228.

XX XX

(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

Adams J, Cory S, Gibson L, Koentgen F, Print C;

XPI: 1999-243890/20.

P-PSDB; AAY05532.

An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w

Disclosure; Page 36; 52pp; English.

The present sequence is described as a derivative of the human bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AAY05532), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation in at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.

Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;

Query Match: 99.1%; Score 578.2; DB 20; Length 583;

Best Local Similarity 99.5%; Pred. No. 3.3e-134;

Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCGACACACAGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
DB 1 ATGGCGACCCAGCCTCGGCCCGACACACAGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
QY 61 AAGCTGAGGAGAGAGGTTATGCTCTGGAGCTGGCCCGGAGGGCCAGCAGCTGAC 120
DB 61 AAGCTGAGGAGAGAGGTTATGCTCTGGAGCTGGCCCGGAGGGCCAGCAGCTGAC 120
QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTGACAGCCGGTCCGGGCGACC 180
DB 121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTGACAGCCGGTCCGGGCGACC 180
QY 181 TTCTGTATCTGGCGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 240
DB 181 TTCTGTATCTGGCGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 240
QY 241 CAGGTTCTCGACAGAACTTTTCAAGGGGGCCCAACTGGGGCGGCTTGTAGCTTCTT 300
DB 241 CAGGTTCTCGACAGAACTTTTCAAGGGGGCCCAACTGGGGCGGCTTGTAGCTTCTT 300
QY 301 GTCTTTGGGGCTCAGCTGTGCTGAGATGTCAACAAGAGATGNAACCACTGTGGA 360
DB 301 GTCTTTGGGGCTCAGCTGTGCTGAGATGTCAACAAGAGATGNAACCACTGTGGA 360
QY 361 CAAGTGCAGGAGTGGATGTGGCTACCTGGAGACCGGCTGCTGACTGATCCACAGC 420
DB 361 CAAGTGCAGGAGTGGATGTGGCTACCTGGAGACCGGCTGCTGACTGATCCACAGC 420
QY 421 AGTGGGGGCTGGCGGAGTTTACAGCTCTATACGGGGACGGGCGCTTGGAGGAGCGCG 480
DB 421 AGTGGGGGCTGGCGGAGTTTACAGCTCTATACGGGGACGGGCGCTTGGAGGAGCGCG 480
QY 481 CGTCTCGGGAGGGAACTGGGATCAGTGAGACAGTCTGACGGGGGCCCTGGCAGTG 540
DB 481 CGTCTCGGGAGGGAACTGGGATCAGTGAGACAGTCTGACGGGGGCCCTGGCAGTG 540
QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTGAA 583

DB 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTGAA 583

RESULT 8

AAX25132

ID AAX25132 standard; DNA; 581 BP.

XX AC AAX25132;

XX XX

XX 05-JUL-1999 (first entry)

XX XX

XX Human bcl-w gene.

XX XX

XX Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;

XX KW animal model; ss.

XX XX

XX Homo sapiens.

XX XX

XX MO9913710-A1.

XX XX

XX 25-MAR-1999.

XX XX

XX 16-SEP-1998; 98MO-AUG0764.

XX XX

XX 16-SEP-1997; 97AU-0009228.

XX XX

XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX XX

XX Adams J, Cory S, Gibson L, Koentgen F, Print C;

XX XX

XX WPI; 1999-243890/20.

XX DR

XX P-PSDB; AAY05530.

XX PT

XX An animal model exhibiting reduced levels of a Bcl-w protein and/or

XX PT

XX protein associated with Bcl-w

XX PS

XX Claim 3; Page 32; 52pp; English.

XX XX

XX The present sequence is the human bcl-w gene encoding Bcl-w protein;

XX CC

XX (see AAY05530), a pro-survival member of the Bcl-2 family which is

XX CC

XX widely expressed and which is essential for spermatogenesis. The

XX CC

XX invention relates generally to a method of treatment and to an

XX CC

XX animal model for the identification of molecules and genetic

XX CC

XX sequences useful for inducing or reducing fertility of male

XX CC

XX animals. Methods are provided for the treatment of infertility, or

XX CC

XX for reducing fertility, by modulating spermatogenesis. An animal

XX CC

XX model carries a mutation in at least one allele of the human or

XX CC

XX murine bcl-w gene or in a gene associated with bcl-w. Such animals

XX CC

XX have disorganised seminiferous tubules and are substantially

XX CC

XX infertile, but possess no other major abnormalities as determined

XX CC

XX by histological examination. They can be used to screen for

XX CC

XX therapeutic molecules including genetic sequences capable of

XX CC

XX inducing, enhancing or otherwise facilitating spermatogenesis in

XX CC

XX animals, or which can induce infertility.

XX SQ

XX Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 other;

Query Match: 99.1%; Score 577.8; DB 20; Length 581;

Best Local Similarity 99.7%; Pred. No. 4.1e-134;

Matches 579; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCGACACACAGGGCTCTGGTGGCAGACTTTGTAGTTAT 60

DB 1 ATGGCGACCCAGCCTCGGCCCGACACACAGGGCTCTGGTGGCAGACTTTGTAGTTAT 60

QY 61 AAGCTGAGGAGAGAGGTTATGCTCTGGAGCTGGCCCGGAGGGCCAGCAGCTGAC 120

DB 61 AAGCTGAGGAGAGAGGTTATGCTCTGGAGCTGGCCCGGAGGGCCAGCAGCTGAC 120

QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGAGCCCGCTTCCGGGCGACC 180

DB 121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGAGCCCGCTTCCGGGCGACC 180

```
QY 181 TTCTCTGATCTGGCGGCTCAGCTGTCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
|||
Db 181 TTCTCTGATCTGGCGGCTCAGCTGTCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
|||
QY 241 CAGGTCTCCGAGCACTTTTCAAGGGGCCCCAACTGGGGCGGCTTGTAGCCCTCTTTT 300
|||
Db 241 CAGGTCTCCGAGCACTTTTCAAGGGGCCCCAACTGGGGCGGCTTGTAGCCCTCTTTT 300
|||
QY 301 GTCTTTGGGGCTGCACTGTGCTGAGAGTGTCACCAAGGAGATGGAACCACTGGTGGGA 360
|||
Db 301 GTCTTTGGGGCTGCACTGTGCTGAGAGTGTCACCAAGGAGATGGAACCACTGGTGGGA 360
|||
QY 361 CAAGTCAGAGTGGATGGTGGCTTCAAGCTCTATACGGGGAGCGGCGCTGGAGAGCGCGG 480
|||
Db 361 CAAGTCAGAGTGGATGGTGGCTTCAAGCTCTATACGGGGAGCGGCGCTGGAGAGCGCGG 480
|||
QY 421 AGTGGGGCTGGGGAGTTCACAGCTCTATACGGGGAGCGGCGCTGGAGAGCGCGG 480
|||
Db 421 AGTGGGGCTGGGGAGTTCACAGCTCTATACGGGGAGCGGCGCTGGAGAGCGCGG 480
|||
QY 481 CGTCTCGGGAGGGAACTGGGCATCAGTAGGACAGTCTCAGCGGGGCGGCGCTGGAGAGCGCGG 540
|||
Db 481 CGTCTCGGGAGGGAACTGGGCATCAGTAGGACAGTCTCAGCGGGGCGGCGCTGGAGAGCGCGG 540
|||
QY 541 GGGGCGCTGGTAACTGTAGGGGCTTTTGTAGCAAGTG 581
|||
Db 541 GGGGCGCTGGTAACTGTAGGGGCTTTTGTAGCAAGTG 581
|||
```

RESULT 9
AAV28334
ID AAV28334 standard; cDNA; 579 BP.

XX AAV28334;
XX
XX
XX 02-OCT-1998 (first entry)
XX Human bcl-y gene.
XX ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.

XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
CDS 1..579
FT /*tag= a
FT /product= bcl-y
FT /note= "No stop codon given"

XX US5789201-A.
PN
XX
XX 04-AUG-1998.
XX
XX 11-FEB-1997; 97US-0798897.
XX
XX 23-FEB-1996; 96US-0012201.
XX 11-FEB-1997; 97US-0798897.
XX
XX (COCE-) COCENSYS INC.
XX
XX Guastella J;
PI
XX
XX WPI; 1998-446079/38.
XX P-PSDB; AAW61392.

XX Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT producing recombinant protein for use in treating uncontrolled cell
PT growth e.g. cancers
XX
XX Claim 3; Column 15/16; 27pp; English.
XX
XX The mammalian bcl-y genes encode a protein that is a member of the bcl-2

CC family, components in the cell death pathway. The bcl-2 family
CC have both apoptotic activity and the apoptosis blocking activity. bcl-y
CC falls in the apoptosis activity category. The recombinant protein may
CC be used to prevent uncontrolled cell growth, either by its direct
CC administration to recombinant genetic constructs to increase its
CC expression in vivo. Also, antisense constructs can be used in disorders
CC where prevention of cell death is desired.

XX SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

Query Match 98.2%; Score 572.6; DB 19; Length 579;
Best Local Similarity 99.3%; Pred. No. 8.1e-133;
Matches 579; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCGACCCAGCCTCGGCCAGACACACCGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
|||
Db 1 ATGCGACCCAGCCTCGGCCAGACACACCGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
|||
QY 61 AAGCTGAGGCGAGAGGTTATGTCTGTGGAGCTTGGCCCCGGGAGGCCAGAGCTGAC 120
|||
Db 61 AAGCTGAGGCGAGAGGTTATGTCTGTGGAGCTTGGCCCCGGGAGGCCAGAGCTGAC 120
|||
QY 121 CCGTGTGCACCAAGCCATGGCGGCAGCTGGAGATGAGTTCCAGACCCGCTTCCGCGCAC 180
|||
Db 121 CCGTGTGCACCAAGCCATGGCGGCAGCTGGAGATGAGTTCCAGACCCGCTTCCGCGCAC 180
|||
QY 181 TTCTCTGATCTGGCGGCTCAGCTGTCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
|||
Db 181 TTCTCTGATCTGGCGGCTCAGCTGTCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
|||
QY 241 CAGGTCTCCAGCACTTTTCAAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
|||
Db 241 CAGGTCTCCAGCACTTTTCAAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
|||
QY 301 GTCTTTGGGGCTGCACCTGTCTGAGAGTGTCAACAAGGAGATGGAAACCACTGGTGGGA 360
|||
Db 301 GTCTTTGGGGCTGCACCTGTCTGAGAGTGTCAACAAGGAGATGGAAACCACTGGTGGGA 360
|||
QY 361 CAAGTCAGAGTGGATGGTGGCTTCAAGCTCTATACGGGGAGCGGCGCTGGAGAGCGCGG 420
|||
Db 361 CAAGTCAGAGTGGATGGTGGCTTCAAGCTCTATACGGGGAGCGGCGCTGGAGAGCGCGG 420
|||
QY 421 AGTGGGGCTGGGGAGTTCACAGCTCTATACGGGGAGCGGCGGCGGCGGCGGCGGCGG 480
|||
Db 421 AGTGGGGCTGGGGAGTTCACAGCTCTATACGGGGAGCGGCGGCGGCGGCGGCGGCGG 480
|||
QY 481 CGTCTGGGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCGGCGGCGGCGG 540
|||
Db 481 CGTCTGGGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCGGCGGCGGCGG 540
|||
QY 541 GGGGCGCTGGTAACTGTAGGGGCTTTTGTAGCAAG 579
|||
Db 541 GGGGCGCTGGTAACTGTAGGGGCTTTTGTAGCAAG 579
|||

RESULT 10

AAV15946
ID AAV15946 standard; cDNA; 579 BP.

XX AAV15946;

XX 20-MAY-1999 (first entry)

XX cDNA encoding the human bcl-y protein.

XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW parasite; ss.

```

XX CS Homo sapiens.
XX PN US5883229-A.
XX PD 16-MAR-1999.
XX PF 25-NOV-1997; 97US-0978523.
XX PR 23-FEB-1996; 96US-0012201.
XX PR 11-FEB-1997; 97US-0798897.
XX PR 25-NOV-1997; 97US-0978523.
XX PA (COCE-) COCENSYS INC.
XX PI Guastella J;
XX DR WPI; 1999-214150/18.
XX DR P-PSDB; AAW97392.
XX PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
XX PT for modulating programmed cell death
XX PS Disclosure; Columns 15-16; 26pp; English.
XX CC The present sequence encodes human bcl-y protein (Hbcl-y). The
XX CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and
XX CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
XX CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
XX CC proteins may be used to treat conditions associated with a disruption of
XX CC the cell death pathway. If they act as cell death inhibitors, they may be
XX CC used in therapies to treat subjects suffering from: strokes, head trauma,
XX CC Alzheimer's Disease, neural and muscular degenerative diseases
XX CC (especially multiple sclerosis), myocardial infarction, vitally induced
XX CC cell death, aging, spinal cord injuries and amyotrophic lateral
XX CC sclerosis- conditions where cells under go premature cell death as a
XX CC result of triggers which may or may not be apparent. They may also be
XX CC used in this way to develop cell lines which remain viable in culture for
XX CC an extended period. In contrast, if they act as cell death stimulators,
XX CC Rbcl-y and Hbcl-y may be used to treat conditions associated with
XX CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and
XX CC lung cancer) and auto/hyperimmune diseases. They may also be used to
XX CC cause cell death in, and hence control, parasites.
XX SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

Query Match 98.2%; Score 572.6; DB 20; Length 579;
Best Local Similarity 99.3%; Pred. No. 8.1e-133;
Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGGGACCCAGCCTCGGCCCCAGACACACAGGGCTCTGTGGGAGACTTTGTAGTTAT 60
DB |||||||
DB 1 ATGGGACCCAGCCTCGGCCCCAGACACACAGGGCTCTGTGGGAGACTTTGTAGTTAT 60
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DB |||||||
DB 61 AAGCTGAGCGAGAGGGTTATCTGTGTGAGTGTGCGCCCGGGAGGCCAGCAGCTGAC 120
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DB 121 CCACTGCACCAAGCCATCGGGCAGCTCGAGATGAGTTCTGAGACCCCGCTTCGGCGCAC 180
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QY 241 CAGGTCTCGAGCAACTTTTCAAGGGGSCCCCACTGGGCGGCTGTAGGCTTCTT 300
DB |||||||
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361 CAAGTSCAGAGTGGATGCTGCCCTACCTGAGAGACCGCGCTGGCTGACTGGATCCACAGC 420
421 AGTGGGGGCTGGCGGAGTTTACAGCTCTATACGGGACCGGGCCCTGGAGAGCGCGG 480
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481 CGTCTCGGGGAGGGGAACCTGGGCATCAGTGAGGACAGTCTCTACCGGGGCCCTGGCACTG 540
481 CGTCTCGGGGAGGGGAACCTGGGCATCAGTGAGGACAGTCTCTACCGGGGCCCTGGCACTG 540
541 GGCGCCCTGTAACCTGTAGGGGCCCTTTTGTGTAGCAAG 579
541 GGCGCCCTGTAACCTGTAGGGGCCCTTTTGTGTAGCAAG 579

RESULT 11
AAV28333
ID AAV28333 standard; cDNA; 579 BP.
XX AC AAV28333;
XX DT 02-OCT-1998 (first entry)
XX DE Rat bcl-y gene.
XX KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX OS Rattus sp.
XX FH Key Location/Qualifiers
XX CDS 1..579
XX FT /*tag= a
XX FT /product= bcl-y
XX FT /note= "No stop codon given"
XX PN US579201-A.
XX PD 04-AUG-1998.
XX PF 11-FEB-1997; 97US-0798897.
XX PR 23-FEB-1996; 96US-0012201.
XX PR 11-FEB-1997; 97US-0798897.
XX PA (COCE-) COCENSYS INC.
XX PI Guastella J;
XX DR WPI; 1998-446079/38.
XX DR P-PSDB; AAW61391.
XX PT Nucleic acids encoding B-cell lymphoma-y protein - useful for
XX PT producing recombinant protein for use in treating uncontrolled cell
XX PT growth e.g. cancers
XX PS Claim 2; Column 13/14; 27pp; English.
XX CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2
XX CC family, components in the cell death pathway. The bcl-2 family
XX CC have both apoptotic activity and the apoptosis blocking activity. bcl-y
XX CC falls in the apoptosis activity category. The recombinant protein may
XX CC be used to prevent uncontrolled cell growth, either by its direct
XX CC administration to recombinant genetic constructs to increase its
XX CC expression in vivo. Also, antisense constructs can be used in disorders
XX CC where prevention of cell death is desired.
XX SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;

Query Match 90.5%; Score 527.8; DB 19; Length 579;
Best Local Similarity 94.5%; Pred. No. 1.1e-121;

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Matches 547; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 1 ATGGGACCCCAAGCCTCGGCCCCAGACACACACGGGCTCTGGTGACAGCTTTGTAGTAT 60
DB |||||
1 ATGGGACCCCAAGCCTCAACCCCAAGACACACACGGGCTCTAGTGGCTGACTTTGTAGCTAT 60
QY 61 AAGCTGAGGAGAGAGGTTATGCTCTGGAGCTGGCCCGGGAGGCGCCAGCAGCTGAC 120
DB |||||
61 AAGCTGAGGAGAGAGGTTATGCTCTGGAGCTGGCCCTGGGAGAGGCCAGCAGCGGAC 120
QY 121 CCCTGACCAAGCCATCGGGGAGCTGAGAGTGTGAGACCGCTTCGGGGCACC 180
DB |||||
121 CCCTGACCAAGCCATCGGGGAGCTGGAGAGTGTGAGACCGCTTCGGGGCACC 180
QY 181 TTCTTGATCTGGGCTCAGCTGATGTGATGACCCAGGCTCAGCCAGAAAGCTTTCAC 240
DB |||||
181 TTCTTGATCTGGGCTCAGCTGATGTGATGACCCAGGCTCAGCCAGAAAGCTTTCAC 240
QY 241 CAGGTCTCCGACCAACTTTTCAAGGGGCCCCCAACTGGGGCCGCTTGTGGCATTC 300
DB |||||
241 CAGGTCTCCGACCAACTTTTCAAGGGGCCCCCAACTGGGGCCGCTTGTGGCATTC 300
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DB |||||
301 GTCTTTGGGCTCGACTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGTGG 360
QY 361 CAAGTCAGAGTGGATGTGGCTACCTGGAGACGGGCTGGCTGACTGGATCCACAGC 420
DB |||||
361 CAAGTCAGAGTGGATGTGGCTACCTGGAGACGGGCTGGCTGACTGGATCCACAGC 420
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DB |||||
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QY 481 CGTCTCGGAGGGGAACTGGGCATCTAGTGAGGACAGTGCCTGACGGGGCGCTGGCA 540
DB |||||
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RESULT 12
AAK15945
ID AAK15945 standard; cDNA; 579 BP.
XX AC AAK15945;
XX DT 20-MAY-1999 (first entry)
XX DE cDNA encoding the rat bcl-y protein.
XX KW Rat bcl-y protein; Bcl-Y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
XX OS Rattus sp.
XX PN US5883229-A.
XX PD 16-MAR-1999.
XX PF 25-NOV-1997; 97US-0978523.
XX PR 23-FEB-1996; 96US-0012201.
XX PR 11-FEB-1997; 97US-0798897.
XX PR 25-NOV-1997; 97US-0978523.
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```
XX (COCE-) COCENSYS INC.
PA Guastella J;
XX KPI; 1999-214150/18.
XX P-PSDB; AAM97391.
XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful
XX for modulating programmed cell death
XX Disclosure; Columns 13-16; 25pp; English.
XX The present sequence encodes rat bcl-y protein (Bcl-y). The
XX specification also describes human bcl-y protein (Hbcl-y). Bcl-y and
XX Hbcl-y are homologues of the bcl-2 protein thought to be involved in
XX programmed cell death (apoptosis and necrosis). Bcl-y and Hbcl-y
XX proteins may be used to treat conditions associated with a disruption of
XX the cell death pathway. If they act as cell death inhibitors, they may be
XX used in therapies to treat subjects suffering from: strokes, head trauma,
XX Alzheimer's disease, neural and muscular degenerative diseases
XX (especially multiple sclerosis), myocardial infarction, vitally induced
XX cell death, aging, spinal cord injuries and amyotrophic lateral
XX sclerosis- conditions where cells under go premature cell death as a
XX result of triggers which may or may not be apparent. They may also be
XX used in this way to develop cell lines which remain viable in culture for
XX an extended period. In contrast, if they act as cell death stimulators,
XX Bcl-y and Hbcl-y may be used to treat conditions associated with
XX prolonged cell life span such as cancer (especially Kaposi's sarcoma and
XX lung cancer) and auto/hyperimmune diseases. They may also be used to
XX cause cell death in, and hence control, parasites.
XX Sequence 579 BP; 111 A; 157 C; 138 G; 113 T; 0 other;
XX Query Match 90.5%; Score 527.8; DB 20; Length 579;
XX Best Local Similarity 94.5%; Pred. No. 1.1e-121;
XX Matches 547; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 1 ATGGGACCCCAAGCCTCGGCCCCAGACACACGGGCTCTGGTGAGAGCTTTGTAGTAT 60
DB |||||
1 ATGGGACCCCAAGCCTCAACCCCAAGACACACGGGCTCTAGTGGCTGACTTTGTAGCTAT 60
QY 61 AAGCTGAGGAGAGGTTATGCTCTGGAGCTGGCCCGGGAGGCGCCAGCAGCTGAC 120
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DB |||||
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QY 421 AGTGGGGCTGGGGAGTTTCAGAGTGTATACGGGAGCGGGCCCTGGAGGAGGACCG 480
DB |||||
421 AGTGGGGCTGGGGAGTTTCAGAGTGTATACGGGAGCGGGCCCTGGAGGAGGACCG 480
QY 481 CGTCTCGGAGGGGAACTGGGCATCTAGTGAGGACAGTGCCTGACGGGGCGCTGGCA 540
DB |||||
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QY 541 GGGGCGCTGGTAACCTGTAGGGGCTTTTCTAGCAG 579
 DB 541 GGGGCGCTGGTAACCTGTAGGGGCTTTTCTAGCAG 579

RESULT 13
 ID AAX25133 standard; DNA; 581 BP.
 AC AAX25133;
 DT 05-JUL-1999 (first entry)
 XX Mouse bcl-w gene.
 DE
 XX
 XX
 XX
 KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
 KW animal model; ss.
 XX
 OS Mus sp.
 XX
 XX WO9913710-A1.
 PD 25-MAR-1999.
 XX
 XX 16-SEP-1999; 98WC-AU00764.
 PF 16-SEP-1997; 97AU-0009228.
 PR 16-SEP-1997; 97AU-0009228.
 XX
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA
 PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
 XX
 XX WPI; 1999-243890/20.
 DR P-PSDB; AAY05531.
 XX
 XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w
 XX
 PS Claim 3; Page 34; 52pp; English.

The present sequence is the mouse bcl-w gene encoding Bcl-w protein
 (see AAY0531), a pro-survival member of the Bcl-2 family which is
 widely expressed and which is essential for spermatogenesis. The
 invention relates generally to a method of treatment and to an
 animal model for the identification of molecules and genetic
 sequences useful for inducing or reducing fertility of male
 animals. Methods are provided for the treatment of infertility, or
 for reducing fertility, by modulating spermatogenesis. An animal
 model carries a mutation is at least one allele of the human or
 murine bcl-w gene or in a gene associated with bcl-w. Such animals
 have disorganised seminiferous tubules and are substantially
 infertile, but possess no other major abnormalities as determined
 by histological examination. They can be used to screen for
 therapeutic molecules including genetic sequences capable of
 inducing, enhancing or otherwise facilitating spermatogenesis in
 animals, or which can induce infertility.

Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 other;

Query Match 90.3%; Score 526.6; DB 20; Length 581;
 Best Local Similarity 94.1%; Pred No. 2.2e-121;
 Matches 547; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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 DB 421 AGTGGGGCTGGCGGAGTTTCAAGCTCTATACGGGACGGGGCCCTGGAGGAGCGCGG 480
 QY 481 CGTCTCGGAGGGGAACTGGGCTCAGTGAGGACAGTGTGACGGGGCCCTGGAGGAGCG 540
 DB 481 CGTCTCGGAGGGGAACTGGGCTCAGTGAGGACAGTGTGACGGGGCCCTGGAGGAGCG 540
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 DB 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTAGCAAGTG 581

RESULT 14
 ID AAT96578 standard; DNA; 581 BP.
 XX
 AC AAT96578;
 XX
 DT 22-APR-1998 (first entry)
 XX
 DE Mouse bcl-w DNA.
 XX
 KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
 KW diagnosis; degenerative disease; ss.
 XX
 OS Mus sp.
 FH Key Location/Qualifiers
 CDS 1..507
 FT /*tag= a
 FT /product= bcl-w
 FT /note= "q"
 XX
 XX WO9735971-A1.
 XX 32-OCT-1997.
 XX
 XX 27-MAR-1997; 97WO-AU00199.
 XX
 XX 27-MAR-1996; 96AU-0008965.
 XX
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX
 XX Adams JM, Cory S, Gibson LM, Holmgren SP;
 XX
 XX WPI; 1997-489635/45.
 XX P-PSDB; AAW36048.
 XX
 XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce
 PT or inhibit cell survival, e.g. for treatment of cancer and
 PT degenerative diseases
 XX
 PS Claim 3; Page 50-51; 86pp; English.

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Qy	241	CAGGTCTCCGACGAACCTTTTCAAGGGGGGCCCAACTGGGGCGCCTTGACGCTTCTTT	300
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QY 541 GGGGCCCTGGTAACTGTAGGGCCCTTTTCTAGCAAGTG 581
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Job time : 179.152 secs

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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:53:10 ; Search time 43.5373 Seconds
(without alignments)
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Title: US-09-925-674A-6

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1.39956

Minimum DB seq length: 6
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	572.6	98.2	579	1	US-08-798-897-2 Sequence 2, Appli
2	572.6	98.2	579	2	US-08-978-523-2 Sequence 2, Appli
3	527.8	90.5	579	1	US-08-798-897-1 Sequence 1, Appli
4	527.8	90.5	579	2	US-08-978-523-1 Sequence 1, Appli
5	428.4	73.5	1864	4	US-09-149-476-130 Sequence 130, Appl
6	131	22.5	926	1	US-08-081-448-5 Sequence 5, Appli
7	131	22.5	926	2	US-08-470-670A-6 Sequence 6, Appli
8	131	22.5	926	3	US-08-481-739-1 Sequence 1, Appli
9	131	22.5	926	3	US-09-167-921-1 Sequence 1, Appli
10	131	22.5	926	3	US-09-277-020-39 Sequence 39, Appli
11	131	22.5	926	3	US-09-323-743-1 Sequence 1, Appli
12	131	22.5	926	4	US-08-461-511A-6 Sequence 6, Appli
13	131	22.5	926	4	US-09-271-014A-5 Sequence 5, Appli
14	131	22.5	926	5	PCT-US94-07089-6 Sequence 6, Appli
15	123.4	21.2	717	2	US-08-465-485A-20 Sequence 20, Appli
16	123.4	21.2	717	3	US-09-080-285-20 Sequence 20, Appli
17	123.4	21.2	4825	6	5459251-1 Patent No. 5459251
18	123.4	21.2	5086	2	US-08-465-485A-19 Sequence 19, Appli
19	123.4	21.2	5086	2	US-08-365-486A-14 Sequence 14, Appli
20	123.4	21.2	5086	3	US-09-080-285-19 Sequence 19, Appli
21	123.4	21.2	5086	3	US-08-880-342-14 Sequence 14, Appli
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23	123.4	21.2	5086	4	US-09-233-527-7 Sequence 7, Appli
24	123.4	21.2	5086	5	PCT-US93-05651-4 Sequence 4, Appli
25	123.4	21.2	5086	5	PCT-US93-06251-2 Sequence 2, Appli
26	123.4	21.2	5094	4	US-09-234-186-7 Sequence 7, Appli
27	123.4	21.2	5104	6	5506344-1 Patent No. 5506344

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29 120.4 20.7 1384 4 US-08-899-367-1 Sequence 1, Appli
30 120.2 20.6 1846 2 US-08-365-486A-16 Sequence 16, Appli
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32 119 20.4 615 2 US-08-465-485A-22 Sequence 22, Appli
33 119 20.4 615 3 US-09-080-285-22 Sequence 22, Appli
34 119 20.4 911 3 US-09-126-109-5 Sequence 5, Appli
35 119 20.4 911 5 PCT-US93-06251-3 Sequence 3, Appli
36 115.8 19.9 831 6 5459251-3 Patent No. 5459251
37 115.8 19.9 831 6 5506344-4 Patent No. 5506344
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ALIGNMENTS

RESULT 1
US-08-798-897-2
; Sequence 2, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.C.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DCS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.01400001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-08-798-897-2

Query Match 98.2%; Score 572.6; DB 1; Length 579;
Best Local Similarity 99.3%; Pred. No. 8.3e-140;
Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATGGCAGCCCCGCTCGGCCCGCCAGACACACAGCGGCTCTGTCGACAGCTTTAGGTTAT 60
Db 1 ATGGCAGCCCCGCTCGGCCCGCCAGACACACAGCGGCTCTGTCGACAGCTTTAGGTTAT 60
Qy 61 AAGCTGAGGCAGAAAGGTTATGTCTGTGGAGCTGGCCCGGGGAGCGGCCAGCGTGCAC 120

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Db 61 AAGCTGAGGACAGAGGTTATGCTGAGAGCTGCCCCGGGAGGCGCCAGAGCTGAC 120
QY 121 CCGCTGACCAAGCAGCAGCTCGGGAGCTGGAGATGAGTTCGAGACCCGCTTCGGCGCACC 150
Db 122 CCAGTGCACCAAGCAGCAGCTCGGGAGCTGGAGATGAGTTCGAGACCCGCTTCGGCGCACC 180
QY 181 TTCTCTGATCTGGGGGCTCAGCTGCATGTCGATGTCACCCAGGCTCAGCCAGCAACGTTTCACC 240
Db 182 TTCCTGATCTGGGGCTCAGCTGCATGTCGATGTCACCCAGGCTCAGCCAGCAACGTTTCACC 240
QY 241 CAGGTCTCCGAGCAACATTTTCAAGGGGGGCCCAACTCGGGGCCCTTTAGGCTTTCTT 300
Db 241 CAGGTCTCCGAGCAACATTTTCAAGGGGGGCCCAACTCGGGGCCCTTTAGGCTTTCTT 300
QY 301 GTCTTTGGGGCTGCACTGTGCTGAGAGTGTCAACAGAGGAGATGGAACCACTGCTGGGA 360
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QY 361 CAAGTGAGGAGTGGATGCTGGCCCTACCTGAGAGCGCGGCTGGCTGATCGATCCACAGC 420
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QY 421 AGTGGGGCTGGGCGGAGTTTCAAGCTCTATACGGGAGCGGGCCCTGGAGGAGCGCGG 480
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QY 481 COTCTCGGGAGGGGAACTGGGCACTCAGTGAGGACAGTGTGACGGGGGCGCTGGCACTG 540
Db 481 COTCTCGGGAGGGGAACTGGGCACTCAGTGAGGACAGTGTGACGGGGGCGCTGGCACTG 540
QY 541 GGGGCCCTGCTAACTGTAGGGGCCCTTTTCTAGCAAG 579
Db 541 GGGGCCCTGCTAACTGTAGGGGCCCTTTTCTAGCAAG 579
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RESULT 2

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US-08-978-523-2
; Sequence 2, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978.523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/978,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-08-978-523-2

Query Match 98.2%; Score 572.6; DB 2; Length 579;
Best Local Similarity 99.3%; Pred. No. 8.3e-140;
Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGGCGAGCCCGAGCCCTCGGCCCGCCAGACACACGGGCTCTGTGGCGAGACTTGTAGTTAT 60
Db 1 ATGGCGAGCCCGAGCCCTCGGCCCGCCAGACACACGGGCTCTGTGGCGAGACTTGTAGTTAT 60
QY 61 AGCTGAGGACAGAGGTTATGCTGTGAGCTGCGCCCGGGAGGCGGCCAGAGCTGAC 120
Db 61 AGCTGAGGACAGAGGTTATGCTGTGAGCTGCGCCCGGGAGGCGGCCAGAGCTGAC 120
QY 121 CCGCTGACCAAGCAGCAGCTCGGGAGCTGGAGATGAGTTCGAGACCCGCTTCGGCGCACC 180
Db 121 CCGCTGACCAAGCAGCAGCTCGGGAGCTGGAGATGAGTTCGAGACCCGCTTCGGCGCACC 180
QY 181 TTCTCTGATCTGGGGGCTCAGCTGCATGTCGATGTCACCCAGGCTCAGCCAGCAACGTTTCACC 240
Db 181 TTCTCTGATCTGGGGGCTCAGCTGCATGTCGATGTCACCCAGGCTCAGCCAGCAACGTTTCACC 240
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Db 241 CAGGTCTCCGAGCAACATTTTCAAGGGGGGCCCAACTCGGGGCCCTTTAGGCTTTCTT 300
QY 301 GTCTTTGGGGCTGCACTGTGCTGAGAGTGTCAACAGAGGAGATGGAACCACTGCTGGGA 360
Db 301 GTCTTTGGGGCTGCACTGTGCTGAGAGTGTCAACAGAGGAGATGGAACCACTGCTGGGA 360
QY 361 CAAGTGAGGAGTGGATGCTGGCCCTACCTGAGAGCGCGGCTGGCTGATCGATCCACAGC 420
Db 361 CAAGTGAGGAGTGGATGCTGGCCCTACCTGAGAGCGCGGCTGGCTGATCGATCCACAGC 420
QY 421 AGTGGGGCTGGGCGGAGTTTCAAGCTCTATACGGGAGCGGGCCCTGGAGGAGCGCGG 480
Db 421 AGTGGGGCTGGGCGGAGTTTCAAGCTCTATACGGGAGCGGGCCCTGGAGGAGCGCGG 480
QY 481 COTCTCGGGAGGGGAACTGGGCACTCAGTGAGGACAGTGTGACGGGGGCGCTGGCACTG 540
Db 481 COTCTCGGGAGGGGAACTGGGCACTCAGTGAGGACAGTGTGACGGGGGCGCTGGCACTG 540
QY 541 GGGGCCCTGCTAACTGTAGGGGCCCTTTTCTAGCAAG 579
Db 541 GGGGCCCTGCTAACTGTAGGGGCCCTTTTCTAGCAAG 579
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RESULT 3

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US-08-978-897-1
; Sequence 1, Application US/08978897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn: Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-08-978-897-1

Query Match 90.5%; Score 527.8; DB :; Length 579;
Best Local Similarity 94.5%; Pred. No. 3.6e-128;
Matches 547; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 1 ATGGGACCCAGCCTCGGCTCCAGACACACAGGGCTCTGGTGGAGACTTTGTAGGTTAT 60
DB 1 ATGGGACCCAGCCTCAACCCAGACACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
QY 61 AAGCTGAGCAGAAAGGTTATGCTGTGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 120
DB 61 AAGCTGAGCAGAAAGGTTATGCTGTGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 120
QY 121 CCGCTSCACCAAGCCATCGGCGAGCTGAGATGATGACCCAGGCTCAGCCAGCAACGCTTACC 180
DB 121 CCGCTSCACCAAGCCATCGGCGAGCTGAGATGATGACCCAGGCTCAGCCAGCAACGCTTACC 180
QY 181 TTCTCTGATCTGGCGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 181 TTCTCTGATCTGGCGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 CAGGTTCCGACGAACTTTTCAAGGGGCGCCCAACTGGGGCGGCTTTGTAGCCTTCTTT 300
DB 241 CAGGTTCCGACGAACTTTTCAAGGGGCGCCCAACTGGGGCGGCTTTGTAGCCTTCTTT 300
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DB 361 CAAGTCAGAGTGGATGGTGGCTACCTGAGACAGCGGCTGGCTGACTGGATCCACAGC 420
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QY 541 GGGGCGCTGCTACTAGGGGCTTTTGTAGCAAG 579
DB 541 GGGGCGCTGCTACTAGGGGCTTTTGTAGCAAG 579

RESULT 4
US-08-978-523-1
Sequence 1, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2

TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-08-978-523-1

Query Match 90.5%; Score 527.8; DB 2; Length 579;
Best Local Similarity 94.5%; Pred. No. 3.6e-128;
Matches 547; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 1 ATGGGACCCAGCCTCGGCTCCAGACACACAGGGCTCTGGTGGAGACTTTGTAGGTTAT 60
DB 1 ATGGGACCCAGCCTCAACCCAGACACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
QY 61 AAGCTGAGCAGAAAGGTTATGCTGTGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 120
DB 61 AAGCTGAGCAGAAAGGTTATGCTGTGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 120
QY 121 CCGCTSCACCAAGCCATCGGCGAGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 180
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EARLIER APPLICATION NUMBER: 60/056,631;
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 73.5%; Score 428.4; DB 4; Length 1864;
Best Local Similarity 99.3%; Pred. No. 3.3e-102;
Matches 429; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
1 ATGGCGACCCAGCGCTCGGCGGCTCTCGTGGCAGACTTTGTAGGTTAT 60
|||||

Db 11 ATGGCGACCCAGCGCTCGGCGGCTCTCGTGGCAGACTTTGTAGGTTAT 70
Qy 61 AAGCTGAGCGCAGAAGGGTTATGTCTGTGGAGTGGCCCGGGAGGGGCCAGCAGCTGAC 120
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Db 131 CCCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCTGAGACCGGCTTCCGGGCGACC 190
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Db 191 TTCTGTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 250
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Qy 361 CAAGTCAGGAGTGGATGTGCGCTTACCTGGAGACGCGGCTGCTGACTGGATCCACAGC 420
Db 371 CAAGTCAGGAGTGGATGTGCGCTTACCTGGAGACGCGGCTGCTGACTGGATCCACAGC 430
Qy 421 AGTGGGGGCTGG 432
Db 431 AGTGGGGGCTGG 442
RESULT 6
US-08-081-448-5
; Sequence 5, Application US/08081448
; Patent No. 5646008
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5646008th Clark Street, Suite 800
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentir Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,448
; FILING DATE: 19930622
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646008thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-744-0090
; TELEFAX: 312-755-4489
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: 135..836
US-08-081-448-5

Query Match 22.5%; Score 131; DB 1; Length 926;
Best Local Similarity 56.3%; Pred. No. 4.5e-25;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 CCGGGAGGGCCAGCAGCTGACCCGCTGACCAAGCCATGCGGCGAGCTGGAGATGAGT 157
DB 364 CCGGGAGGGTATCCCATGGCAGCAGTAAAGCAAGCGTGAGGAGGCGGCGAGT 423
QY 158 TCGAGACCGCTTCCGGCGACCTTCTCTGATCTGCGGCTCAGCTGATGTGACCCAG 217
DB 424 TTGAATCGGGTACCGCGGCGATTCAGTGACCTGACATCCCGCTCCACATCACCCAG 483
QY 218 GCTAGCCCGCAGCAAGCTTACCCAGGCTTCCGACGAACTTTTCAAGGGGGCCCCAACT 277
DB 484 GCACAGCATATCAGAGCTTTGAACAGGTTAGTGAATGAATCTTCCGGGATGGGTAACT 543
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DB 544 GGGGTGCGATTGTGGCTTTTCTCTTCCGCGGCGCACTGTGCGTGGAAAGCGTAGACA 603
QY 338 AGGAGATGGAACCACTGTGTGGGCAAGTGCAGAGTGGATGTGGCTTACCTGGAGACGC 397
DB 604 AGGAGATGCAAGTATGGTGAGTGGATCGGAGCTTGGATGGCCACTTACCTGAATGACC 663
QY 398 GGCTGGCTGACTGATCCACAGCAGTGGGGCTGGGGGAGTTTACAGCTTCTATACGGGG 457
DB 664 ACCTAGAGCTTGGATCCAGGAGAACGGGGCTGGGATACTTTTGTGGAATCTATGGGA 723
QY 458 ACGGGGCGCTGGAGAGGCGCGGCTTCCGGGAGGGGAACCTGGGCATCAGTGAGGACAG 517
DB 724 ACAATGACAGCCGAGAGCGGAAAGGCGGCACTGTGCGTGGAAAGCGTAGACA 603
QY 518 TGCTGACGGGGCGG 532
DB 784 GCATGACTGTGGCGG 798

RESULT 7
US-08-470-670A-6
; Sequence 6, Application US/08470670A
; Patent No. 5834309
; Patent No. 5834309 5710045
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B. B.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,670A
; FILING DATE:
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/09,448
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander Steven L.
; REGISTRATION NUMBER: 37,642

; REFERENCE/DOCKET NUMBER: ARCD:090--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; US-08-470-670A-6

Query Match 22.5%; Score 131; DB 2; Length 926;
Best Local Similarity 56.3%; Pred. No. 4.5e-25;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 CCGGGAGGGCCAGCAGCTGACCCGCTGACCAAGCCATGCGGCGAGCTGGAGATGAGT 157
DB 364 CCGGGAGGGTATCCCATGGCAGCAGTAAAGCAAGCGTGAGGAGGCGGCGAGT 423
QY 158 TCGAGACCGCTTCCGGCGACCTTCTCTGATCTGCGGCTCAGCTGATGTGACCCAG 217
DB 424 TTGAATCGGGTACCGCGGCGATTCAGTGACCTGACATCCCGCTCCACATCACCCAG 483
QY 218 GCTAGCCCGCAGCAAGCTTACCCAGGCTTCCGACGAACTTTTCAAGGGGGCCCCAACT 277
DB 484 GCACAGCATATCAGAGCTTTGAACAGGTTAGTGAATGAATCTTCCGGGATGGGTAACT 543
QY 278 GGGGCGGCTTGTAGCTTCTTTGTTTGGGCTTGCATGTGTGCTGAGAGTGTCAACA 337
DB 544 GGGGTGCGATTGTGGCTTTTCTCTTCCGCGGCGCACTGTGCGTGGAAAGCGTAGACA 603
QY 338 AGGAGATGGAACCACTGTGTGGGCAAGTGCAGAGTGGATGTGGCTTACCTGGAGACGC 397
DB 604 AGGAGATGCAAGTATGGTGAGTGGATCGGAGCTTGGATGGCCACTTACCTGAATGACC 663
QY 398 GGCTGGCTGACTGATCCACAGCAGTGGGGCTGGGGGAGTTTACAGCTTCTATACGGGG 457
DB 664 ACCTAGAGCTTGGATCCAGGAGAACGGGGCTGGGATACTTTTGTGGAATCTATGGGA 723
QY 458 ACGGGGCGCTGGAGAGGCGCGGCTTCCGGGAGGGGAACCTGGGCATCAGTGAGGACAG 517
DB 724 ACAATGACAGCCGAGAGCGGAAAGGCGGCACTGTGCGTGGAAAGCGTAGACA 603
QY 518 TGCTGACGGGGCGG 532
DB 784 GCATGACTGTGGCGG 798

RESULT 8
US-08-481-739-1
; Sequence 1, Application US/08481739
; Patent No. 6143291
; GENERAL INFORMATION:
; APPLICANT: June, Carl H. and Thompson, Craig B.
; TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
; TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/481,739
;; FILING DATE: 07-JUNE-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/435,518
;; FILING DATE: 04-MAY-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DeConti, Giulio A. (GAD)
;; REGISTRATION NUMBER: 31,503
;; REFERENCE/DOCKET NUMBER: RPI-034CP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)742-4214
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 926 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 135..836
US-08-481-739-1

Query Match 22.5%; Score 131; DB 3; Length 926;
Best Local Similarity 56.3%; Pred. No. 4.5e-25;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 CCGGGAGGGCCAGCAGCTGACCCGCTGCAACAGCCATCGGCGAGCTGGAGATGAGT 157
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Db 364 CCGGGAGGTGATCCCATGGCAGCAGTAAAGCAAGCGCTGAGGAGGCGAGCGAGT 423

QY 158 TCGAGACCCGCTTCGGGGCCACCTTCTCTGATCTGGGGCTCAGCTGCATGTACCCAG 217
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Db 424 TTGAATCGGGTACCGCGCGGATTCAGTGACCTGACATCCAGCTCCACATCACCCAG 483

QY 218 GCTAGACCCAGCAACGCTTCACCCAGGCTTCGAGCGAACTTTTCAAGGGGGCCCCAAT 277
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Db 484 GGACACATATCAGAGCTTTGAACAGGTAGTGAATGAATCTTCGGGATGGGTAACT 543

QY 278 GGGGGCGCTTGAGCCTTCTTGTCTTTGGGGCTGCACTGTGCTGAGAGTGTCAACA 337
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Db 544 GGGTTCGATTTGGCTTTTCTCTTCGGGGCGGACTGTGGTGAAGCGTAGACA 603

QY 338 AGGAGATGAACCATGTGGTGACAAAGTGCAGGAGTGGTGGCTTACCTGAGAGCG 397
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Db 604 AGGAGATGAGGTATTGGTGAATCGGATCGCAGCTTGGATGGCACTTACCTGAATGACC 663

QY 398 GGCTGGCTGACTGATCCACAGCAGTGGGGGCTGGGGGAGTTTACAGCTCTATACGGG 457
|||
Db 664 ACCTAGAGCTTTGGATCCAGAGAGCGCGCTGGGATACTTTGTGGAATCTTATGGGA 723

QY 458 ACGGGCCCTTGAGAGGAGCGCGCTCTCGGGAGGGGAACCTGGGCACTCAGTGAGAGAG 517
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Db 724 ACAATGACAGCCGAGAGCGGAGCGGAGGAGCGGAGGAGCGCTTCAACCGCTGGTCTCAGCG 783

QY 518 TGCTGACGGGGCCG 532
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Db 784 GCATGACTGGGCG 798

RESULT 9
US-09-167-921-1
; Sequence 1, Application US/09167921A
; Patent No. 6172216
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, Qingqing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression

;; FILE REFERENCE: ISPH-0324
;; CURRENT APPLICATION NUMBER: US/09/167,921A
;; CURRENT FILING DATE: 1998-10-07
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1
;; LENGTH: 926
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (135)..(836)
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: L20121 Genbank
;; DATABASE ENTRY DATE: 1994-07-26
US-09-167-921-1

Query Match 22.5%; Score 131; DB 3; Length 926;
Best Local Similarity 56.3%; Pred. No. 4.5e-25;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 CCGGGAGGGCCAGCAGCTGACCCGCTGCAACAGCCATCGGCGAGCTGGAGATGAGT 157
|||
Db 364 CCGGGAGGTGATCCCATGGCAGCAGTAAAGCAAGCGCTGAGGAGGCGAGCGAGT 423

QY 158 TCGAGACCCGCTTCGGGGCCACCTTCTCTGATCTGGGGCTCAGCTGCATGTACCCAG 217
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Db 424 TTGAATCGGGTACCGCGCGGATTCAGTGACCTGACATCCAGCTCCACATCACCCAG 483

QY 218 GCTAGACCCAGCAACGCTTCACCCAGGCTTCGAGCGAACTTTTCAAGGGGGCCCCAAT 277
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QY 278 GGGGGCGCTTGAGCCTTCTTGTCTTTGGGGCTGCACTGTGCTGAGAGTGTCAACA 337
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Db 544 GGGTTCGATTTGGCTTTTCTCTTCGGGGCGGACTGTGGTGAAGCGTAGACA 603

QY 338 AGGAGATGAACCATGTGGTGACAAAGTGCAGGAGTGGTGGCTTACCTGAGAGCG 397
|||
Db 604 AGGAGATGAGGTATTGGTGAATCGGATCGCAGCTTGGATGGCACTTACCTGAATGACC 663

QY 398 GGCTGGCTGACTGATCCACAGCAGTGGGGGCTGGGGGAGTTTACAGCTCTATACGGG 457
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Db 664 ACCTAGAGCTTTGGATCCAGAGAGCGCGCTGGGATACTTTGTGGAATCTTATGGGA 723

QY 458 ACGGGCCCTTGAGAGGAGCGCGCTCTCGGGAGGGGAACCTGGGCACTCAGTGAGAGAG 517
|||
Db 724 ACAATGACAGCCGAGAGCGGAGCGGAGGAGCGGAGGAGCGCTTCAACCGCTGGTCTCAGCG 783

QY 518 TGCTGACGGGGCCG 532
|||
Db 784 GCATGACTGGGCG 798

RESULT 10
US-09-277-020-39
; Sequence 39, Application US/09277020
; Patent No. 6210892
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
; TITLE OF INVENTION: of mRNA Processing
; FILE REFERENCE: ISPH-0339
; CURRENT APPLICATION NUMBER: US/09/277,020
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/167,921
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-277-020-39

Query Match 22.5%; Score 131; DB 3; Length 926;
Best Local Similarity 56.3%; Pred. No. 4.5e-25;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;
QY 98 CCGGGAGGGCCAGCAGCTGACCCGCTGCACCAAGCCATCGGGGAGCTGGAGATGAGT 157
DB 364 CCGGGAGGTGATCCCATGCGCAGCAGTAAGCAAGCGCTGAGGGAGCGAGGAGT 423
QY 158 TCGAGACCGCTTCGGGCGCAGCTTCTCTGATCTGGGCGCTGAGTGTGACCCAG 217
DB 424 TTGAACGTGCGGTACCGGGCGCATTCAGTGACCTCCAGCTCCACATCACCAG 483
QY 218 GCTCAGCCAGCAACGCTTCAACCGAGTCTCCGAGCAACTTTTCAAGGGGCCCCAACT 277
DB 484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTTCCGGATGGGTAACT 543
QY 278 GGGGCGGCTTGTAGCCTTCTTTGCTTTGGGGCTGCACCTGTGCTGAGTGTCAACA 337
DB 544 GGGGTGCAATTTGGCCCTTTTCTCTTCCGCGGGGCACTGTGCTGGAAGCGTAGACA 603
QY 338 AGGAGATGGAACCACTGCTGGGCAAGTGCAGGAGTGGATGGTGGCTTACCTGGAGACG 397
DB 604 AGGAGATGCAAGTATTGGTAGTGGATCGCAGCTTGGATGGCCACTTACTGATGACC 563
QY 398 GGCTGGCTGACTGGATCCACAGCTGGGGCTGGGCGGAGTTACAGCTCTATACGGGG 457
DB 664 ACCTAGAGCCTTGGATCCAGGAGAACGGCGCTGGGATACITTTCTGGAACCTCTATGGA 723
QY 458 ACGGGGCGCTGGAGAGCGCGGCTGTGCGGAGGGGAACTGGGCATCAGTGAGGACAG 517
DB 724 ACAATGCAAGCGCGAGAGCGGAAAGGCGGCAAGCTTCAACCGCTGTTCTGTGACG 783
QY 518 TGCTGACGGGGCGG 532
DB 784 GCATGACTGTGGCGG 798

RESULT 11

US-09-323-743-1
; Sequence 1, Application US/09123743
; Patent No. 6214986
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nikoloff, Brian J.
; APPLICANT: Zhang, QingQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0368
; CURRENT APPLICATION NUMBER: US/09/323.743
; EARLIER FILING DATE: 1999-06-01
; EARLIER FILING DATE: 1999-07-020
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 09/167,921
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)...(836)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26

Query Match 22.5%; Score 131; DB 3; Length 926;
Best Local Similarity 56.3%; Pred. No. 4.5e-25;

Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;
QY 98 CCGGGAGGGCCAGCAGCTGACCCGCTGCACCAAGCCATCGGGGAGCTGGAGATGAGT 157
DB 364 CCGGGAGGTGATCCCATGCGCAGCAGTAAGCAAGCGCTGAGGGAGCGAGGAGT 423
QY 158 TCGAGACCGCTTCCGGGCGCAGCTTCTCTGATCTGGGCGCTGAGTGTGACCCAG 217
DB 424 TTGAACGTGCGGTACCGGGCGCATTCAGTGACCTCCAGCTCCACATCACCAG 483
QY 218 GCTCAGCCAGCAACGCTTCAACCGAGTCTCCGAGCAACTTTTCAAGGGGCCCCAACT 277
DB 484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAATCTTCCGGATGGGTAACT 543
QY 278 GGGGCGGCTTGTAGCCTTCTTTGCTTTGGGGCTGCACCTGTGCTGAGTGTCAACA 337
DB 544 GGGGTGCAATTTGGCCCTTTTCTCTTCCGCGGGGCACTGTGCTGGAAGCGTAGACA 603
QY 338 AGGAGATGGAACCACTGCTGGGCAAGTGCAGGAGTGGATGGTGGCTTACCTGGAGACG 397
DB 604 AGGAGATGCAAGTATTGGTAGTGGATCGCAGCTTGGATGGCCACTTACTGATGACC 563
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DB 724 ACAATGCAAGCGCGAGAGCGGAAAGGCGGCAAGCTTCAACCGCTGTTCTGTGACG 783
QY 518 TGCTGACGGGGCGG 532
DB 784 GCATGACTGTGGCGG 798

RESULT 12
US-08-461-511A-6
; Sequence 6, Application US/08461511A
; Patent No. 630331
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.3C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,511A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: UNKNOWN
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

PCT-US94-07089-6

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Query Match      22.5%; Score 131; DB 5; Length 926;
Best Local Similarity 56.3%; Pred. No. 4.5e-25;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 CCGGGAGGGCCAGCAGCTGACCGCTGACCAAGCCATCGGGGAGCTGAGATGAGT 157
DB 364 CCGGGAGGTATCCCATGCGCAGCAGTAAAGCAAGCGCTGAGGAGGCGAGCGAGT 423
QY 158 TCGAGACCGCTTCGGGCGCACCTTCTCTGATCTGGGGCTCAGCTGATGACCCAG 217
DB 424 TGAAGTGGGTACCGGGGCAATTCAGTACCTGACATCCAGCTCCATCACCAG 483
QY 218 GCTCAGCCAGCAACGCTTCAACCCAGGTCTCCGACGAACTTTTCAAGGGGCCCAACT 277
DB 484 GGCACAGCATATCAGAGCTTGAACAGGTAGTGAATGAATCTTCCGGGATGGGGTAACT 543
QY 278 GGGGCGGCTTGAGCTCTTTGCTTCTTGGGCTGACATGCTGCTGAGAGTCTACACA 337
DB 544 GGGGTGCGATGTTGGCTTTTCTCTTCCGCGGGCAGCTGTGGTGGAAAGCGTAGACA 603
QY 338 AGGAGATGAACCACTGGTGGGACAAAGTCAGGAGTGGATGTGCTTACCTGAGAGCG 397
DB 604 AGGAGATGAGATTTGGTGGTGGATCGGATCGCAGCTTGGATGGCCACTTACCTGATGACC 663
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DB 664 ACCTAGAGCTTGGATCCAGGAGAACGGCGGTGGATACTTTTGGAACTCTATGGGA 723
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DB 724 ACAAATGACAGCCGAGAGCGGAAAGGCGCAGGAGCTTCAACCGCTGGTTCCTGACGG 783
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DB 784 GCATGACTGGGCGG 798
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RESULT 15

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US-08-465-485A-20
Sequence 20, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
Applicant: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
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ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..717
US-08-465-485A-20
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Best Local Similarity 58.8%; Pred. No. 4e-23;
Matches 214; Conservative 0; Mismatches 151; Indels 0; Gaps 0;
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QY 211 ACCCGAGGCTCAGCCAGCAACGCTTCCAGCAGCTTCCGACGAACTTTTTCAGGGGGC 270
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DB 424 GTGAATGGGGAGGATTTGGGCTTCTTTGATTCGGTGGGTCAATGTGTGGAGAGC 483
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DB 484 GTCAACCGGGAGATGTGCGCCCTGTGGACAAACATCGCCCTGTGGATGACTGAGTACCTG 543
QY 391 GAGACGGGCTGCTGACTGGATCCACAGCAGTGGGGCTGGGCGGAGTTCACAGCTCTA 450
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QY 451 TACGG 455
DB 604 TACGG 608
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Job time : 45.5373 secs
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GenCore version: 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 13:01:31 ; Search time 162.639 Seconds
(without alignments)
9613.225 Million cell updates/sec

Title: US-09-925-674A-6

Perfect score: 583
Sequence: 1 atggcgaccagctcgccg.....ctttttgctagcaagtgaa 583

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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- 3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq.*
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- 6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	428.2	73.4	578	12	US-10-029-386-10549
6	427.2	73.3	433	12	US-10-029-386-24249
7	257	44.1	6049	12	US-10-311-455-201
8	223	38.3	6049	12	US-10-311-455-202
9	152	26.1	590	12	US-10-029-386-13384
10	151	25.9	151	12	US-10-029-386-27084
11	150	25.7	150	9	US-09-864-761-17690
12	131	22.5	636	12	US-10-169-223-13
13	131	22.5	702	11	US-09-959-987-9
14	131	22.5	926	9	US-09-734-846-1
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17	131	22.5	926	12	US-10-302-262-1	Sequence 1, Appli
18	131	22.5	926	14	US-10-072-830-3	Sequence 3, Appli
19	123.4	21.2	717	12	US-10-053-645A-23	Sequence 20, Appli
20	123.4	21.2	5086	8	US-08-726-211-4	Sequence 4, Appli
21	123.4	21.2	5086	12	US-10-141-618-11	Sequence 11, Appli
22	123.4	21.1	600	9	US-09-864-761-7360	Sequence 7360, Ap
23	122.2	21.0	555	9	US-09-864-761-24081	Sequence 24081, A
24	122.2	21.0	564	12	US-10-029-386-20790	Sequence 20790, A
25	121.8	20.9	1050	14	US-10-072-830-1	Sequence 1, Appli
26	121.8	20.9	6030	12	US-10-007-926A-117	Sequence 117, App
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28	121.8	20.9	6142	14	US-10-198-846-13703	Sequence 13703, A
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32	119	20.4	911	8	US-08-726-211-6	Sequence 6, Appli
33	115.4	19.8	1303	10	US-09-952-278-1	Sequence 1, Appli
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36	60.2	10.3	65	12	US-09-908-975-2435	Sequence 2435, Ap
37	52.6	9.0	737	10	US-09-952-278-7	Sequence 7, Appli
38	52.2	9.0	65	12	US-09-908-975-28692	Sequence 28692, A
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41	50.2	8.6	573	14	US-10-196-793A-45	Sequence 45, Appli
42	50.2	8.6	579	12	US-09-908-147-10	Sequence 10, Appli
43	50.2	8.6	579	12	US-09-908-147-18	Sequence 18, Appli
44	50.2	8.6	579	12	US-10-306-878-4	Sequence 4, Appli
45	50.2	8.6	624	14	US-10-277-693A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-925-674A-6

; Sequence 6, Application US/09925674A

; Patent No. US20020119943A1

; GENERAL INFORMATION:

; APPLICANT: AMRAD Operations Pty Ltd

; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2

; FILE REFERENCE: 11686a

; CURRENT APPLICATION NUMBER: US/09/925,674A

; CURRENT FILING DATE: 2001-08-09

; PRIOR APPLICATION NUMBER: 09/925,674

; PRIOR FILING DATE: 2001-08-09

; PRIOR APPLICATION NUMBER: P88965

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 583

; TYPE: DNA

; ORGANISM: HUMAN

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(579)

US-09-925-674A-6

Query Match: 100.0%; Score 583; DB 10; Length 583;

Best Local Similarity: 100.0%; Pred. No. 1.9e-150;

Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTTGGCAGACTTTGTAGGTTAT 60

Db 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTTGGCAGACTTTGTAGGTTAT 60

QY 61 AAGCTGAGGCGAGGCTTATGCTGTGGAGCTGCGCCCGGGAGGCCCGCCAGAGCTGAC 120

Db 61 AAGCTGAGGCGAGGCTTATGCTGTGGAGCTGCGCCCGGGAGGCCCGCCAGAGCTGAC 120

QY 121 CCGCTGCACCAAGCCATCGGGGAGCTGGAGATGAGTTCGAGACCCCGCTTCCGGCGCACC 180

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Db 121 CCGCTGCAACCAAGCATCGCGGACGTCGAGATGATGTCGAGACCCGCTTCGGCGCAC 180
Qy 181 TTCCTGATCTGGGGCTCAGCTGATGTAGACCCAGGCTCAGCCAGCAGCAGCTTCACC 240
Db 181 TTCCTGATCTGGGGCTCAGCTGATGTAGACCCAGGCTCAGCCAGCAGCAGCTTCACC 240
Qy 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGGCCCGCTTTGAGCCCTCTTT 300
Db 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGGCCCGCTTTGAGCCCTCTTT 300
Qy 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGGAGATGGAACCACTGGTGGGA 360
Db 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGGAGATGGAACCACTGGTGGGA 360
Qy 361 CAAGTGCAGGAGTGTGATGCTGCTTACCTGAGAGCGCGCTGGCTGACTGGATCCACAGC 420
Db 361 CAAGTGCAGGAGTGTGATGCTGCTTACCTGAGAGCGCGCTGGCTGACTGGATCCACAGC 420
Qy 421 AGTGGGGCTGGGGGAGTTCACAGCTCTATACGGGACCGGGCCCTGGAGGAGCGCGG 480
Db 421 AGTGGGGCTGGGGGAGTTCACAGCTCTATACGGGACCGGGCCCTGGAGGAGCGCGG 480
Qy 481 CGTCTGGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 540
Db 481 CGTCTGGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 540
Qy 541 GGGGCCCTGGCTAACTGTAGGGGCTTTTGTAGCAAGTGA 583
Db 541 GGGGCCCTGGCTAACTGTAGGGGCTTTTGTAGCAAGTGA 583
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RESULT 2
US-09-925-674A-8
; Sequence 8, Application US/09925674A
; Patent No., US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11686a
; CURRENT FILING DATE: 2001-08-09
; PRIOR FILING DATE: 2001-08-09
; PRIOR FILING DATE: 2001-08-09
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: {1}..(579)
US-09-925-674A-8
Query Match 89.9%; Score 524.4; DB 10; Length 582;
Best Local Similarity 93.8%; Pred. No. 2,3e-134;
Matches 546; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
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Qy 1 ATGGGACCCCGAGCTCGCCCCAGACACACCGGGTCTGTGGCAGACTTTGTAGTTAT 60
Db 1 ATGGGACCCCGAGCTCAACCCAGACACACCGGGTCTGTGGCAGACTTTGTAGTTAT 60
Qy 61 AAGCTGAGCAGAGAGGTTATGCTGTGAGCTGCCCCGGGGAGGGCCAGCAGCTGAC 120
Db 61 AAGCTGAGCAGAGAGGTTATGCTGTGAGCTGCCCCGGGGAGGGCCAGCAGCTGAC 120
Qy 121 CGCTGCACCAAGCCATGCGGCAGCTGAGATGAGTTCGAGACCCGCTTCGGGGCACC 180
Db 121 CGCTGCACCAAGCCATGCGGCAGCTGAGATGAGTTCGAGACCCGCTTCGGGGCACC 180
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Qy 181 TTCCTGATCTGGCGCTCAGCTGATGTAGACCCAGGCTCAGCCAGCAGCAGCTTCACC 240
Db 181 TTCCTGATCTGGCGCTCAGCTGATGTAGACCCAGGCTCAGCCAGCAGCAGCTTCACC 240
Qy 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGGCCCGCTTTGAGCCCTCTTT 300
Db 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGGCCCGCTTTGAGCCCTCTTT 300
Qy 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGGAGATGGAACCACTGGTGGGA 360
Db 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGGAGATGGAACCACTGGTGGGA 360
Qy 361 CAAGTGCAGGAGTGTGATGCTGCTTACCTGAGAGCGCGCTGGCTGACTGGATCCACAGC 420
Db 361 CAAGTGCAGGAGTGTGATGCTGCTTACCTGAGAGCGCGCTGGCTGACTGGATCCACAGC 420
Qy 421 AGTGGGGCTGGGGGAGTTCACAGCTCTATACGGGAGCGGGCCCTGGAGGAGCGCGG 480
Db 421 AGTGGGGCTGGGGGAGTTCACAGCTCTATACGGGAGCGGGCCCTGGAGGAGCGCGG 480
Qy 481 CGTCTGGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 540
Db 481 CGTCTGGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 540
Qy 541 GGGGCCCTGGCTAACTGTAGGGGCTTTTGTAGCAAGTGA 582
Db 541 GGGGCCCTGGCTAACTGTAGGGGCTTTTGTAGCAAGTGA 582
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RESULT 3
US-09-809-391-13C
; Sequence 130, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1648)
; OTHER INFORMATION: n equals a.t.g, or c
US-09-809-391-130
Query Match 73.5%; Score 428.4; DB 11; Length 1864;
Best Local Similarity 99.3%; Pred. No. 5.5e-108;
Matches 429; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 ATGGGACCCCGAGCTCGCCCCAGACACACCGGGTCTGTGGCAGACTTTGTAGTTAT 60
Db 11 ATGGGACCCCGAGCTCGCCCCAGACACACCGGGTCTGTGGCAGACTTTGTAGTTAT 70
Qy 61 AAGCTGAGGAGAGAGGTTATGCTGTGAGCTGCCCCGGGGAGGGCCAGCAGCTGAC 120
Db 71 AAGCTGAGGAGAGAGGTTATGCTGTGAGCTGCCCCGGGGAGGGCCAGCAGCTGAC 130
Qy 121 CCGGTGCACCAAGCCATGCGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGGCACC 180
Db 131 CCGGTGCACCAAGCCATGCGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGGCACC 190
Qy 181 TTCCTGATCTGGCGCTCAGCTGATGTAGACCCAGGCTCAGCCAGCAGCAGCTTCACC 240
Db 191 TTCCTGATCTGGCGCTCAGCTGATGTAGACCCAGGCTCAGCCAGCAGCAGCTTCACC 250
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QY 241 CAGGTCTCGACGAACCTTTTCAAGGGGGCCCCCAACTGGGCGGCTTGTAGCCTCTTT 300
 Db |||||
 251 CAGGTCTCGATGAACCTTTTCAAGGGGGCCCCCAACTGGGCGGCTTGTAGCCTCTTT 310
 QY 301 GTCCTTGGGGCTGCACCTGTGCTGAGAGTGTCACAAGGAGATGGAACCACTGGTGGGA 360
 Db |||||
 311 GTCCTTGGGGCTGCACCTGTGCTGAGAGTGTCACAAGGAGATGGAACCACTGGTGGGA 370
 QY 361 CAAGTCAGAGTGGATGGTGGCTTACTCTGGAGAGCGGCTGGCTGACTGGATCCACAGC 420
 Db |||||
 371 CAAGTCAGAGTGGATGGTGGCTTACTCTGGAGAGCGGCTGGCTGACTGGATCCACAGC 430
 QY 421 AGTGGGGGCTGG 432
 Db |||||
 431 AGTGGGGGCTGG 442

RESULT 4

US-09-882-171-130
 ; Sequence 130, Application US/09882171
 ; Publication No. US20030175858A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: 186 Human Secreted proteins
 ; FILE REFERENCE: P2002P2
 ; CURRENT APPLICATION NUMBER: US/09/882,171
 ; CURRENT FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 09/809,391
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 09/149,476
 ; PRIOR FILING DATE: 1998-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US98/04493
 ; PRIOR FILING DATE: 1998-03-06
 ; PRIOR APPLICATION NUMBER: 60/040,162
 ; PRIOR FILING DATE: 1997-03-07
 ; PRIOR APPLICATION NUMBER: 60/040,333
 ; PRIOR FILING DATE: 1997-03-07
 ; PRIOR APPLICATION NUMBER: 60/038,621
 ; PRIOR FILING DATE: 1997-03-07
 ; PRIOR APPLICATION NUMBER: 60/040,626
 ; PRIOR FILING DATE: 1997-03-07
 ; PRIOR APPLICATION NUMBER: 60/040,334
 ; PRIOR FILING DATE: 1997-03-07
 ; PRIOR APPLICATION NUMBER: 60/040,336
 ; PRIOR FILING DATE: 1997-03-07
 ; PRIOR APPLICATION NUMBER: 60/040,163
 ; PRIOR FILING DATE: 1997-03-07
 ; PRIOR APPLICATION NUMBER: 60/047,600
 ; PRIOR FILING DATE: 1997-05-23
 ; PRIOR APPLICATION NUMBER: 60/047,615
 ; PRIOR FILING DATE: 1997-05-23
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 ; PRIOR FILING DATE: 1997-05-23
 ; PRIOR APPLICATION NUMBER: 60/047,502
 ; PRIOR FILING DATE: 1997-05-23
 ; PRIOR APPLICATION NUMBER: 60/047,633
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 ; PRIOR FILING DATE: 1997-05-23
 ; PRIOR APPLICATION NUMBER: 60/047,613
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 ; PRIOR APPLICATION NUMBER: 60/043,311
 ; PRIOR FILING DATE: 1997-04-11
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 ; PRIOR FILING DATE: 1997-04-11
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 ; PRIOR FILING DATE: 1997-04-11
 ; PRIOR APPLICATION NUMBER: 60/043,313
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 ; PRIOR APPLICATION NUMBER: 60/043,672
 ; PRIOR FILING DATE: 1997-04-11
 ; PRIOR APPLICATION NUMBER: 60/043,315
 ; PRIOR FILING DATE: 1997-04-11
 ; PRIOR APPLICATION NUMBER: 60/048,974
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/056,886
 ; PRIOR FILING DATE: 1997-08-22
 ; PRIOR APPLICATION NUMBER: 60/056,877
 ; PRIOR FILING DATE: 1997-08-22
 ; PRIOR APPLICATION NUMBER: 60/056,889
 ; PRIOR FILING DATE: 1997-08-22
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 ; PRIOR FILING DATE: 1997-08-22
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 ; PRIOR APPLICATION NUMBER: 60/056,894

1 PRIOR FILING DATE: 1997-08-22
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16 PRIOR APPLICATION NUMBER: 60/056,892
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40 PRIOR APPLICATION NUMBER: 60/043,578
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43 PRIOR FILING DATE: 1997-04-11
44 PRIOR APPLICATION NUMBER: 60/047,501
45 PRIOR FILING DATE: 1997-03-23
46 PRIOR APPLICATION NUMBER: 60/043,670
47 PRIOR FILING DATE: 1997-04-11
48 PRIOR APPLICATION NUMBER: 60/056,632
49 PRIOR FILING DATE: 1997-08-22
50 PRIOR APPLICATION NUMBER: 60/056,664
51 PRIOR FILING DATE: 1997-08-22
52 PRIOR APPLICATION NUMBER: 60/056,876
53 PRIOR FILING DATE: 1997-08-22
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56 PRIOR APPLICATION NUMBER: 60/056,909
57 PRIOR FILING DATE: 1997-08-22
58 PRIOR APPLICATION NUMBER: 60/056,875
59 PRIOR FILING DATE: 1997-08-22
60 PRIOR APPLICATION NUMBER: 60/056,862
61 PRIOR FILING DATE: 1997-08-22
62 PRIOR APPLICATION NUMBER: 60/056,887
63 PRIOR FILING DATE: 1997-08-22
64 PRIOR APPLICATION NUMBER: 60/056,908
65 PRIOR FILING DATE: 1997-08-22
66 PRIOR APPLICATION NUMBER: 60/048,964
67 PRIOR FILING DATE: 1997-06-06
68 PRIOR APPLICATION NUMBER: 60/057,650
69 PRIOR FILING DATE: 1997-09-05
70 PRIOR APPLICATION NUMBER: 60/056,884
71 PRIOR FILING DATE: 1997-08-22
72 PRIOR APPLICATION NUMBER: 60/057,669
73 PRIOR FILING DATE: 1997-09-05

Query Match 73.5%; Score 428.4; DB 12; Length 1864;
Best Local Similarity 99.3%; Pred. No. 5.5e-108;
Matches 429; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGGACCCAGCTCGGGCCGACACACACACGGGCTCTGGTGGCAGACTTTAGGTTAT 60
DB |||||
QY 11 ATGGGACCCAGCTCGGGCCGACACACACACGGGCTCTGGTGGCAGACTTTAGGTTAT 70
DB |||||
QY 61 AAGCTGAGGCGAAGAGGTTATGTCTGTGGAGTGGCCCGGGGAGGGCCGACGAGTGC 120
DB |||||
QY 71 AAGCTGAGGCGAAGAGGTTATGTCTGTGGAGTGGCCCGGGGAGGGCCGACGAGTGC 130
DB |||||
QY 121 CCCTGACCAAGCCATCGGGCAGCTGAGAGTTCGAGACCGCTTCGGCGCACCC 180
DB |||||
QY 131 CCCTGACCAAGCCATCGGGCAGCTGAGAGTTCGAGACCGCTTCGGCGCACCC 190
DB |||||
QY 181 TTCTGTGATCTGGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 240
DB |||||
QY 191 TTCTGTGATCTGGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 250
DB |||||
QY 241 CAGGTCTCCGACGAACTTTTCAAGGGGCCCCAACTGGGGGCGGCTTTAGCCTTCTT 300
DB |||||
QY 251 CAGGTCTCCGATGAACTTTTCAAGGGGCCCCAACTGGGGGCGGCTTTAGCCTTCTT 310
DB |||||
QY 301 GTCTTTGGGCTGCATCTGTGCTGAGAGTGTCAACAAGAGATGGAACACTTGGTGGGA 360
DB |||||
QY 311 GTCTTTGGGCTGCATCTGTGCTGAGAGTGTCAACAAGAGATGGAACACTTGGTGGGA 370
DB |||||
QY 361 CAAGTCAGAGTGGATGGTGGCTTACCTGGAGACCGGCTGGCTGACTGGATCCACAGC 420
DB |||||
QY 371 CAAGTCAGAGTGGATGGTGGCTTACCTGGAGACCGGCTGGCTGACTGGATCCACAGC 430
DB |||||
QY 421 AGTGGGGCTGG 432
DB |||||
QY 431 AGTGGGGCTGG 442
DB |||||

RESULT 5
US-10-029-386-10549
; Sequence 10549, Application US/10029386
; Publication No. US200301947041
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10549
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CH14.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUATE 0.00e+00
; OTHER INFORMATION: NT HIT: gi14751151, EVALUATE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALUATE 2.00e-72
US-10-029-386-10549

Query Match 73.4%; Score 428.2; DB 12; Length 578;
Best Local Similarity 99.3%; Pred. No. 5.7e-108;
Matches 430; Conservative 0; Mismatches 3; Indels 0; Gaps 0;


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QY 1 ATGGGAGACCCCTAGCCTCGGCCCCCAAGACACACGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
Db 105 ATGGGACCCCTAGCCTCGGCCCCCAAGACACACGGGCTCTGGTGGCAGACTTTGTAGTTAT 164
QY 61 AAGCTGAGCAGACAGGGTTATCTCTGTGGAGCTGCCCCGGGAGGGCCAGCAGCTGAC 120
Db 165 AAGCTGAGCAGACAGGGTTATCTCTGTGGAGCTGCCCCGGGAGGGCCAGCAGCTGAC 224
QY 121 CGGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGCGCAC 160
Db 225 CGGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGCGCAC 284
QY 181 TTCTCTGATCTGGGGCTCAGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 240
Db 285 TTCTCTGATCTGGGGCTCAGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 344
QY 241 CAGGTCTCCGACGAACTTTTCAAGGGGCCCCAACTGGGGCGGCTTGTAGCCTTCTTT 300
Db 345 CAGGTCTCCGACGAACTTTTCAAGGGGCCCCAACTGGGGCGGCTTGTAGCCTTCTTT 404
QY 301 GTCTTTGGGGCTGCACCTGTGCTCAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
Db 405 GTCTTTGGGGCTGCACCTGTGCTCAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 464
QY 361 CAAGTGCAGGAGTGGATGGTGGCTTACCTGGAGACGGGGCTGGCTGATGATCCACAGC 420
Db 465 CAAGTGCAGGAGTGGATGGTGGCTTACCTGGAGACGGGGCTGGCTGATGATCCACAGC 524
QY 421 AGTGGGGGCTGG 433
Db 525 AGTGGGGGCTGG 537

RESULT 6
US-10-029-386-24249
; Sequence 24249, Application US/10-029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24249
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALUE 2.00e-72
; OTHER INFORMATION: NT HIT: g14751151, EVALUE 0.00e-00
US-10-029-386-24249

Query Match 73.3%; Score 427.2; DB 12; Length 433;
Best Local Similarity 99.3%; Pred. No. 1e-107;
Matches 429; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 61 AAGCTGAGCAGAAAGGGTTATCTGTGTGAGCTGCCCCGGGAGGGCCAGCAGCTGAC 120
Db 62 AAGCTGAGCAGAAAGGGTTATCTGTGTGAGCTGCCCCGGGAGGGCCAGCAGCTGAC 121
QY 121 CGGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGCGCAC 180
Db 222 CGGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGCGCAC 181
QY 181 TTCTCTGATCTGGGGCTCAGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 240
Db 182 TTCTCTGATCTGGGGCTCAGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 241
QY 241 CAGGTCTCCGACGAACTTTTCAAGGGGCCCCAACTGGGGCGGCTTGTAGCCTTCTTT 300
Db 242 CAGGTCTCCGACGAACTTTTCAAGGGGCCCCAACTGGGGCGGCTTGTAGCCTTCTTT 301
QY 301 GTCTTTGGGGCTGCACCTGTGCTCAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
Db 302 GTCTTTGGGGCTGCACCTGTGCTCAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 361
QY 361 CAAGTGCAGGAGTGGATGGTGGCTTACCTGGAGACGGGGCTGGCTGATGATCCACAGC 420
Db 362 CAAGTGCAGGAGTGGATGGTGGCTTACCTGGAGACGGGGCTGGCTGATGATCCACAGC 421
QY 421 AGTGGGGGCTGG 432
Db 422 AGTGGGGGCTGG 433

RESULT 7
US-10-311-455-201
; Sequence 201, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Det
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 201
; LENGTH: 6049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-201

Query Match 44.1%; Score 257; DB 12; Length 6049;
Best Local Similarity 74.6%; Pred. No. 6.4e-61;
Matches 323; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
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QY 1 ATGGCCACCCCGCTCGGGCCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
Db 5001 ATGGCGATTTTGTGTTTGGTTTGTAGATATACCGGTTTGGTGGTAGATTTGTAGGTTAT 5060
QY 61 AAGCTGAGCAGAAAGGGTTATGCTGTGGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 120
Db 5061 AAGTTGAGGTAGAGGGTTATGTTGTGGAGTTGGTTTCGGGGAGGGTTAGTAGTTAT 5120
QY 121 CGGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGCGCAC 180
Db 5121 TCCTTGTATTAACTTATCGGGTAGTTGGAGATGAGTTCGAGATTCGTTTCGGGCTATT 5180
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QY 181 TTCTCTGATCTGGGGCTCAGCTGCATGTGATGCCAGCTCAGCCAGCAACAGCTTCACC 240
DB 5181 TTTTGTATTTGGGGTTTAGTCTGTATGTGATTTTAGTCTTAGTTTAAATACGTTTTATT 5240
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAAGTGGGGCGCTTGTAGCCCTCTTT 300
DB 5241 TAGGTTTCGATGAATTTTAAAGGGGGTTTAAAGGGGGTCTTGTAGTTTGTAGTTT 5300
QY 301 GTCTTTGGGCTGCAGCTGTGCTGAGAGTGTCAACAGAGAGATGGAACCACTGGTGGGA 360
DB 5301 GTTTTGGGGTGTATGCTGTGTTGAGAGTGTAAATAGAGAGATGGAATATTGGTGGGA 5360
QY 361 CAAGTGCAGAGTGTGATGGTCTACCTGAGAGCGCGCTGGCTGACTGGATCCACAGC 420
DB 5361 TAAGTGTAGAGTGTGATGGTCTTATTGGAGACGTAGTGGTGTATTGGATTTATAGT 5420
QY 421 AGTGGGGCTGGG 433
DB 5421 AGTGGGGTGGG 5433

RESULT 8
US-10-311-455-202/c
; Sequence 202, Application US/20311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting
; FILE REFERENCE: 5013.1014
; CURRENT FILING DATE: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 202
; LENGTH: 6049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-202

Query Match 38.3%; Score 223; DB 12; Length 6049;
Best Local Similarity 70.4%; Pred. No. 1.4e-51;
Matches 298; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
QY 1 ATGGCGACCCAGCCTCGGCCCGACACACAGCGGCTCTGGTGGAGACTTTGTAGGTAT 60
DB 1049 ATAAGACCCCACTCGACCCCAACACAGCACTCTAAACAACACTTTATAAATAT 990
QY 61 AAGCTGAGGCGAAGGGTTATGTCTGTGGAGCTGCGCCCGGGAGGCGCCAGAGCTGAC 120
DB 989 AAACATAAACAAAAAATATATCTATAAACTAACCCCGAAAAAACCACCAACAAAC 930
QY 121 CCGCTGACCAAGCATCGGGCGAGATGAGTTCGAGACCGCTTCGGCGGAC 180
DB 929 CCGCTACCAACCAATACGAACTAAATAAATTCGAAACCGCTTCGCGACGAC 870
QY 181 TTCTCTGATCTGGCGGCTCAGCTGTGATGATGATGATGATGATGATGATGATGATGAT 240
DB 859 TTCTCTATCTAACGACTCACTACATATATACCCCAAACTCAACCAACAGCTTCACC 810
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAAGTGGGGCGCTTGTAGCCCTCTTT 300
DB 809 CAATCTCCGATAAACTTTTCAAAAAAACCACCACTAAACCCGCTTATAACCTCTTT 750

QY 301 GTCTTTGGGGCTCAGCTGTGCTGAGAGTGTCAACAGAGAGATGGAACCACTGGTGGGA 360
DB 749 ATCTTTAAAACTACACTATATATACTAAAAATATCAACAAAAAATAAAACCACTTAATAAAA 690
QY 361 CAAGTGCAGAGTGTGATGGTCTACCTGGAGACGCGCTGGCTGACTGGATCCACAGC 420
DB 689 CAATACAAAAATAAATAAATAACCTTACCTAAAAACGCAACTAACTAACTAAATCCACAAC 630
QY 421 AGT 423
DB 629 AAT 627

RESULT 9
US-10-029-386-13384
; Sequence 13384, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOMICA-X-2
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 13384
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 2.00e-10
; OTHER INFORMATION: NT HIT: g114751151, EVALUE 0.000e+00
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUE 1.00e-119
US-10-029-386-13384

Query Match 26.1%; Score 152; DB 12; Length 590;
Best Local Similarity 100.0%; Pred. No. 3.4e-32;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 432 GCGGAGTTTACAGCTCTATACGGGACGGGCGCTTGGAGAGGCGCGCGCTTCGCGGA 491
DB 25 GCGGAGTTTACAGCTCTATACGGGACGGGCGCTTGGAGAGGCGCGCGCTTCGCGGA 94
QY 492 GGGGAACCTGGGATCAGTCAAGACAGTCTGACGGGGCGCTGGACCTGGGCGCTTGGT 551
DB 85 GGGGAACCTGGGATCAGTCAAGACAGTCTGACGGGGCGCTGGACCTGGGCGCTTGGT 144
QY 552 AACTGTAGGGGCTTTTGTCTAGCAAGTGA 583
DB 145 AACTGTAGGGGCTTTTGTCTAGCAAGTGA 176

RESULT 10
US-10-029-386-27084
; Sequence 27084, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOMICA-X-2
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 27084
LENGTH: 151
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR14.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUE 5.00e-70
OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11
OTHER INFORMATION: NT HIT: g114574571, EVALUE 9.00e-80
US-10-029-386-27084

Query Match 25.9%; Score 151; DB 12; Length 151;
Best Local Similarity 100.0%; Pred. No. 5.8e-32;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 432 GCGGAGTTACAGCTCTATACGGGACGGGCGCTGGAGGCGCGGCTCTGCGGGA 491
DB 1 GCGGAGTTACAGCTCTATACGGGACGGGCGCTGGAGGCGCGGCTCTGCGGGA 60
QY 492 GGGGAACCTGGGATCAGTGAGGACAGTGTCTACGGGGGCGCTGGCACTGGGGGCGCTGGT 551
DB 61 GGGGAACCTGGGATCAGTGAGGACAGTGTCTACGGGGGCGCTGGCACTGGGGGCGCTGGT 120
QY 552 AACTGTAGGGGCGCTTTTGTCTAGCAAGTGA 582
DB 121 AACTGTAGGGGCGCTTTTGTCTAGCAAGTGA 151

RESULT 11
US-09-864-761-17690
Sequence 17690, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aemica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/532,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/638,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 17690
LENGTH: 150
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL049829.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
OTHER INFORMATION: NT HIT: D87461.1, EVALUE 2.00e-79
OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUE 8.00e-70
OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11
US-09-864-761-17690

Query Match 25.7%; Score 150; DB 9; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 433 GCGGAGTTACAGCTCTATACGGGACGGGCGCTGGAGGCGCGGCTCTGCGGGA 492
DB 1 GCGGAGTTACAGCTCTATACGGGACGGGCGCTGGAGGCGCGGCTCTGCGGGA 60
QY 493 GGAACCTGGGATCAGTGAGGACAGTGTCTACGGGGGCGCTGGCACTGGGGGCGCTGGTA 552
DB 61 GGAACCTGGGATCAGTGAGGACAGTGTCTACGGGGGCGCTGGCACTGGGGGCGCTGGTA 120
QY 553 ACTGTAGGGGCGCTTTTGTCTAGCAAGTGA 582
DB 121 ACTGTAGGGGCGCTTTTGTCTAGCAAGTGA 150

RESULT 12
US-10-169-223-13
Sequence 13, Application US/10169223
Publication No. US20030152946A1
GENERAL INFORMATION:
APPLICANT: SHIMIZU, Shigeomi
APPLICANT: TSUJIMOTO, Yoshihide
TITLE OF INVENTION: BH4-Fused Polypeptides
FILE REFERENCE: 1422-0537P
CURRENT APPLICATION NUMBER: US/10/169,223
CURRENT FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: JP 11-371449
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: PCT/JP00/09274
PRIOR FILING DATE: 2000-12-26
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 636
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized DNA for mutant bcl-xL
NAME/KEY: CDS

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; LOCATION: (1)...(636)
; OTHER INFORMATION:
US-10-169-223-13

Query Match      22.5%; Score 131; DB 12; Length 636;
Best Local Similarity 56.3%; Pred. No. 2e-26;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 CCGGGAGGCGCCAGCAGCTGACCCGCTGCACCAAGCCATCGGGCGCAGCTGGAGATGAGT 157
DB 167 CCGGGAGGTGATCCCATGGCAGCAGTAAGCAAGCGCTGAGGAGCGCAGCGCAGT 226
QY 158 TCGAGACCCGCTTCGGGCGACCTTCTCTGATCTGGCGGCTCAGCTGATGTGACCCGAG 217
DB 227 TTGAACCTCGGTACCGGGCGGCAATTCACTGACCTGACATCCAGCTCCACATCAACCCGAG 286
QY 218 GCTCAGCCAGCAACGCTTCACCCAGGCTCCGAGCACTTTTCAAGGGGGCCCCAACT 277
DB 287 GGACGACATATCAGAGCTTTGAACAGGTAGTGAATGAATCTTTCGGGATGGGTAACT 346
QY 278 GGGGCGGCTTGTAGCCTTCTTTGCTTTTGGGCTGCACCTGTGTGTGAGAGTGTCAACA 337
DB 347 GGGGTGCGATTGTGGCCCTTTTCTCTTCGCGGGCGCACTGTGCTGGAAGCCTAGACA 406
QY 338 AGGAGATGGAACCACTGCTGGGCAAGTGCAGGAGTGGATGGTGGCTTACCTGAGAGCG 397
DB 407 AGGAGATGAGGTATTGTGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 466
QY 398 GCCTGGCTGACTGGATCCACAGCAGTGGGGCTGGGCGGAGTTCCACAGCTCTATACGGGG 457
DB 467 ACCTAGAGCTTGTGATCCAGGAGACGCGGCTGGATACCTTTGTGGAATCTATGGGA 526
QY 458 ACGGGGCTTGGAGAGCGCGGCTGTCTGCGGAGGGGAACTGGGCATCAGTGGAGACAG 517
DB 527 ACAATGCAGCAGCGGAGAGCGGAAAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 586
QY 518 TGCTGACGGGGCGCG 532
DB 587 GCATGACTGTGGCGG 601

RESULT 13
US-09-959-987-9
; Sequence 9, Application US/09959987
; Publication No. US20030040012A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Corporation
; TITLE OF INVENTION: A Detection Method of Protein-Protein Interaction
; FILE REFERENCE: 2001.1695A/WMC/03653
; CURRENT APPLICATION NUMBER: US/09/959,987
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/JF01/01973
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(702)
US-09-959-987-9

Query Match      22.5%; Score 131; DB 11; Length 702;
Best Local Similarity 56.3%; Pred. No. 2e-26;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 CCGGGAGGCGCCAGCAGCTGACCGCTGCACCAAGCCATCGGGCGCAGCTGGAGATGAGT 157
DB 230 CCGGGAGGTGATCCCATGGCAGCAGTAAGCAAGCGCTGAGGAGCGCAGCGCAGT 289
QY 158 TCGAGACCCGCTTCGGGCGCAGCTTCTCTGATCTGGCGGCTCAGCTGCAATGTGACCCGAG 217
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DB 290 TTGAACCTCGGTACCGGGCGGCAATTCAGTGACCTGACATCCAGCTCCACATCACCCGAG 349
QY 218 GCTCAGCCAGCAACGCTTCACCCAGGCTCCGAGCACTTTTCAAGGGGGCCCCAACT 277
DB 350 GGACACATATCAGAGCTTTGAACAGGTAGTGAATGAATCTTTCGGGATGGGTAACT 409
QY 278 GGGGCGGCTTGTAGCCTTCTTTGCTTTTGGGCTGCACCTGTGTGTGAGAGTGTCAACA 337
DB 410 GGGGTGCGATTGTGGCCCTTTTCTCTTCGCGGGGCACTGTGCTGGAAGCCTAGACA 469
QY 338 AGGAGATGGAACCACTGCTGGGCAAGTGCAGAGTGGATGGCTTACCTGAGAGCG 397
DB 470 AGGAGATGAGGTATTGTGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 529
QY 398 GCCTGGCTGACTGGATCCACAGCAGTGGGGCTGGGCGGAGTTCCACAGCTCTATACGGGG 457
DB 530 ACCTAGAGCTTGTGATCCAGGAGACGCGGCTGGATACCTTTTGTGGAATCTATGGGA 589
QY 458 ACGGGGCTTGGAGAGCGCGGCTGTCTGCGGAGGGGAACTGGGCATCAGTGGAGACAG 517
DB 590 ACAATGCAGCAGCGGAGAGCGGAAAGGGCGCAGGAACGCTTCAACCGCTGGTTCCTGACGG 649
QY 518 TGCTGACGGGGCGCG 532
DB 650 GCATGACTGTGGCGG 664

RESULT 14
US-09-734-846-1
; Sequence 1, Application US/09734846
; Patent No. US20010007025A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, Qingling
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0528
; CURRENT APPLICATION NUMBER: US/09/734,846
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/323,743
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)...(836)
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
US-09-734-846-1

Query Match      22.5%; Score 131; DB 9; Length 926;
Best Local Similarity 56.3%; Pred. No. 2e-26;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 CCGGGAGGCGCCAGCAGCTGACCCGCTGCACCAAGCCATCGGGCGCAGCTGGAGATGAGT 157
DB 364 CCGGGAGGTGATTCCTCATGGCAGCAGTAAGCAAGCGCTGAGGAGCGCAGCGCAGT 423
QY 158 TCGAGACCCGCTTCGGGCGCAGCTTCTCTGATCTGGCGGCTCAGCTGCAATGTGACCCGAG 217
DB 424 TTGAACCTCGGTACCGGGCGGCAATTCAGTGACCTCCAGCTCCACATCACCCGAG 483
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QY 218 GGTACGCCAGCAACGCTTCAACCGAGGCTCCGACGAACCTTTTCAAGGGGGCCCCAACCT 277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 484 GGACAGCATATCAGAGCTTTGAACAGAGTAGTGAATGAACTCTTCGGGATGGGGTAAACT 543
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 278 GGGCGCGCTTGAGCTCTTGTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAACA 337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 544 GGGTCCGATCTGTGGCTTTTCTCTTCGGCGGGGCACTGTGCGTGGAAAGCGTAGACA 603
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 338 AGGAGATGGAACCACTGGTGGGACAAAGTCAGAGAGTGGATGGTGGCTTACCTGGAGAGCG 397
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 604 AGGAGATGAGGTATTTGGTGGTGGATCGGATCGGAGCTTGGATGGCACTTACCTGATGACC 663
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 398 GGTGTGCTACTGGATCCACAGACAGTGGGGGCTGGGGGAGTTCACAGCTCTATACGGGG 457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 664 ACCTAGAGCCTTGGATCCAGGAGAACGGGGCTGGGATACCTTTTGGAACTCTATGGGA 723
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 458 ACGGGGCCCTGGAGGAGCGCGGCTCTCGGGAGGGGAACCTGGSCATCAGTGGAGACAG 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 724 ACAATGACAGAGCCGAGAGCCGAAAGGGCCAGGAACGCTTCAACCGCTGGTTCTCTGACGG 783
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 518 TGCTGACGGGGCGCG 532
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 784 GCATGACTGTGGCGG 798
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 15

```
US-09-734-847A-39
; Sequence 39, Application US/09734847A
; Patent No. US20020049173A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Monia, Brett P.
; APPLICANT: Freir, Susan
; APPLICANT: McKay, Robert
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation of mRNA
; FILE REFERENCE: ISPH-0524
; CURRENT APPLICATION NUMBER: US/09/734,847A
; CURRENT FILING DATE: 2000-12-12
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-734-847A-39
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Query Match 22.5%; Score 131; DB 9; Length 926;
Best Local Similarity 56.3%; Pred. No. 2e-26;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 CCGGGAGGGCCCGCAGCAGTGCACCCGCTGCACCAAGCCATGCGGCGAGCTGGAGATGAGT 157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 CCGGGAGGGTGATCCCATGGCAGCAGTAAGCAAGCGCTGAGGGAGGCGAGCGAGT 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 158 TCGAGACCCGCTTCGGCGCACCTTCTCTGTATGGGGCTCAGTGCATGTGACCCGAG 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 424 TTGAACCTCGGTACCGCGGGGCAATTCAGTGACCTCCAGATCCAGCTCCACATCAACCCAG 483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 218 GCTCAGCCAGACAGCTTCACCCAGGCTCTCCGCAAGACTTTTCAAGGGGGCCCCAACT 277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 484 GGACAGCATATCAGACTTTGAAACAGGTAGTAATGAATCTTCCGGGATGGGGTAAACT 543
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 278 GGGCGCGCCTTGTAGGCTTCTTTGTGGGCTGCACCTGTGTGCTGAGAGTGTCAACA 337
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Search completed: October 27, 2003, 15:13:30
Job time : 163.639 secs

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Db 544 GGGTCCGCTTGTGGCCTTTTCTCCTTCGGCGGGGCACTGTGCGTGSAAAGCGTAGACA 603
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QY 338 AGGAGATGGAACCACTGGTGGGACAAAGTGCAGAGTGGATGGTGGCTACCTGGAGAGCG 397
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 604 AGGAGATGCAAGGTATTGGTGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 663
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 398 GGTGGCTGACTGGATCCACAGAGTGGGGGCTGGCGGAGTTTCACAGCTCTATACGGGG 457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 664 ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACCTTTTGTGAACTCTATGGGA 723
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 458 ACGGGGCCCTGGAGGAGCGCGGCTCTCGGGAGGGGAACCTGGGCACTCAGTGGAGACAG 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 724 ACAATGACAGAGCCGAGAGCCGAAAGGGCCAGGAACGCTTCAACCGCTGGTTCTCTGACGG 783
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw mode:

Run on: October 27, 2003, 11:50:55 ; Search time 1470.26 Seconds
(without alignments;
9637.411 Million cell: updates/sec

Title: US-09-925-674A-6

Perfect score: 583

Sequence: 1 atggcgaccagctcgtggc.....ctttttgctagcaagtga 583

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estp:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_tod:*

26: em_gss_pbg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554.8	95.2	804	9	AL157542
2	553.2	94.9	1030	10	BE793530
3	527.6	90.5	1349	11	AK015644
4	527.6	90.5	3487	11	AK004680

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	525	90.2	969	14	BY715200
6	488.2	83.7	697	12	BY70566
7	470.4	80.7	967	13	BU503850
8	447.8	76.8	626	14	CA391923
9	422.4	72.5	643	12	BY10270
10	400.2	68.6	815	10	BF785386
11	386.6	66.3	823	14	CB578463
12	380.2	65.2	854	11	AK013244
13	369	63.3	792	10	BG298789
14	364.8	62.6	548	14	CA407899
15	363.8	62.4	869	13	BU557268
16	363.8	62.4	872	13	BU557410
17	362	62.1	540	9	AW258810
18	336.8	57.8	437	14	CB790932
19	336	57.6	440	14	CB749817
20	328.4	56.3	758	12	BY764428
21	322.6	55.3	1053	13	BU931540
22	306.8	52.6	559	14	BY704881
23	295.4	50.7	645	14	BY740551
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25	294.2	50.5	749	10	BG677345
26	294	50.4	410	14	CB804140
27	289.6	49.7	362	9	AA596919
28	284.2	48.7	1064	13	BO646339
29	269.6	46.2	460	13	BY285647
30	266	45.6	449	13	BY253191
31	257.6	44.2	433	9	AW326901
32	257.4	44.2	430	14	CB760687
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34	241.4	41.4	853	14	CA984774
35	240.6	41.3	353	13	BY312773
36	233.2	40.0	425	13	BY251598
37	232.2	39.8	467	13	BY253189
38	229.6	39.4	302	13	BY356166
39	229.2	39.3	452	14	CB786193
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41	217.6	37.3	375	13	BY302913
42	215.6	37.0	372	13	BY133304
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44	208.6	35.8	365	13	BY136977
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ALIGNMENTS

RESULT 1
AL157542
LOCUS
DEFINITION
AL157542
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL157542 804 bp mRNA linear EST 24-FEB-2000
DKFZp761D0816.r1.761 (synonym: hamy2) Homo sapiens cDNA clone
DKFZp761D0816.5', mRNA sequence.

AL157542.1 GI:7057943

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 804)

Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.

EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)

Unpublished

Contact: Ansorge W

MIPS

IngoIsaeder Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by EMBL (European Molecular Biology Laboratories, of the

Heidelberg/Germany) within the cDNA sequencing consortium of the

German Genome Project.

No si sequence available.

This clone (DKFZp761D0816) is available at the R2PD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source
1. 804
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="DKFZP761D0816"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="H101" (synonym: hamy2)"
/note="vector: pspori1; Site_1: NotI; Site_2: SalI"
150 a 217 c 294 g 142 t 1 others

BASE COUNT

ORIGIN

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Query Match      95.2%; Score 554.8; DB 9; Length 804;
Best Local Similarity 99.1%; Pred. No. 6.9e-120;
Matches 578; Conservative C; Mismatches 3; Indels 2; Gaps 2;

QY 1 ATGGCGACCCAGCGCTCGGCCCCAGACACAGCGGCTCTGGTGGCAGACTTTAGGTAT 60
DB 134 ATGGCGACCCAGCGCTCGGCCCCAGACACAGCGGCTCTGGTGGCAGACTTTAGGTAT 133
QY 61 AAGCTGAGGCGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGCCCCAGAGCTGAC 120
DB 194 AAGCTGAGGCGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGCCCCAGAGCTGAC 253
QY 121 CCGCTGCACCAAGCATCGCGGCGAGCTGGAGATGAGTTCGAGACCCGCTTCCGCGCACC 180
DB 254 CCGCTGCACCAAGCATCGCGGCGAGCTGGAGATGAGTTCGAGACCCGCTTCCGCGCACC 313
QY 181 TTCTCTGATCTGGCGGTTCAGCTGCATGTGATACCCAGGCTCAGCCAGAACGCTTCACC 240
DB 314 TTCTCTGATCTGGCGGTTCAGCTGCATGTGATACCCAGGCTCAGCCAGAACGCTTCACC 373
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGGCCCGCTTGTAGCTTCTTT 300
DB 374 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGGCCCGCTTGTAGCTTCTTT 433
QY 391 GTCTTTGGGGTGCACCTGTGTGCTGAGAGTGTCAACAGGAGATGGAACCACTGGTGGGA 360
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QY 361 CAAGTGCAGAGTGGATGGTGGCTTACTTGAGAGCGCGCTGGGTGACTGTGATCCACAGC 420
DB 494 CAAGTGCAGAGTGGATGGTGGCTTACTTGAGAGCGCGCTGGGTGACTGTGATCCACAGC 553
QY 421 AGTGGGGCTGGCGGAGTTTCACAGCTCTATACGGGAGCGGGCCCTGGAGAGGCGCGG 480
DB 554 AGTGGGGCTGGCGGAGTTTCACAGCTCTATACGGGAGCGGGCCCTGGAGAGGCGCGG 612
QY 481 CGTCTCGCGGAGGGGAACTGGGCATCAGTGAAGAGTGTGACGGGGCGCGTGGCACTG 540
DB 613 CGTCTCGCGGAGGGGAACTGGGCATCAGTGAAGAGTGTGACGGGGCGCGTGGCACT- 671
QY 541 GGGGCCCTGGTAACTGTAGGGCCCTTTTGTAGCAAGTAA 583
DB 672 GGGGCCCTGGTAACTGTAGGGCCCTTTTGTAGCAAGTAA 714

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RESULT 2

BE793530
LOCUS
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mRNA sequence.
ACCESSION BE793530
VERSION BE793530.1 GI:10214832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: sgapbs@mail.nih.gov
Tissue Procurement: DCTD/BTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM800 row: P column: 04
High quality sequence start: 5
High quality sequence stop: 709.

FEATURES

source

1. 1030
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/clone_lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
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cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(S). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 190 a 284 c 386 g 170 t

ORIGIN

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Query Match      94.9%; Score 553.2; DB 10; Length 1030;
Best Local Similarity 96.9%; Pred. No. 1.8e-119;
Matches 564; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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DB 144 ATGGCGACCCAGCGCTCGGCCCCAGACACACAGCGGCTCTGGTGGCAGACTTTGTAGTTAT 203
QY 61 AAGCTGAGGCGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGCCCCAGAGCTGAC 123
DB 204 AAGCTGAGGCGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGCCCCAGAGCTGAC 263
QY 121 CGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTTCGAGACCCGCTTCCGGCGCACC 180
DB 264 CCACTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTTCGAGACCCGCTTCCGGCGCACC 323
QY 181 TTCTCTGATCTGGCGGTTCAGCTGCATGTGACCCAGGCTCAGCCAGAACGCTTTCACC 240
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QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGGCCCGCTTGTAGCTTCTTT 300
DB 384 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGGCCCGCTTGTAGCTTCTTT 443
QY 301 GTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
DB 444 GTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 503
QY 361 CAAGTGCAGAGTGGATGGTGGCTTACTTGAGAGCGCGCTGGCTGACTGTGATCCACAGC 420
DB 504 CAAGTGCAGAGTGGATGGTGGCTTACTTGAGAGCGCGCTGGCTGACTGTGATCCACAGC 563
QY 421 AGTGGGGCTGGCGGAGTTTCACAGCTCTATACGGGAGCGGGCCCTGGAGAGGCGCGG 480
DB 564 AGTGGGGCTGGCGGAGTTTCACAGCTCTATACGGGAGCGGGCCCTGGAGAGGCGCGG 623
QY 481 CGTCTCGCGGAGGGGAACTGGGCATCAGTGAAGAGTGTCAACAAGGAGATGGAACCACTGGTGGCACTG 540

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Qy 541 GGGGCGCTGTGTAACCTAGGGGCTTTTGTAGCAAGTGA 582

Db 684 GGGGCGCTGGTAACTGTAGGGGCTTTTGTAGCAAGTGA 725

RESULT 3
 LOCUS AK015644
 DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:493048D08 product:Bc12-like 2, full insert sequence.
 ACCESSION AK015644
 VERSION 1
 KEYWORDS High-efficiency full-length cDNA cloning
 SOURCE Meth. Enzymol. 303, 19-44 (1999)
 ORGANISM Mus musculus (house mouse)

REFERENCE 1
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99273253
 PUBMED 10349636

REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kusunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, K., Fujiwaka, S., Inoue, K., Ozawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ogawa, K., Tanaka, T., Matsura, S., Kawai, S., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE 4
 AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamazaki, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, K., Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, M., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kueh, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schiraldi, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, Y., Aono, H., Badarelli, R., Barsh, G., Blake, J., Boiffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kotsuki, S. and Hayashizaki, Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851

REFERENCE 5

AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 1949)
 AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, J., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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 BASE COUNT 396 a 473 c 628 g 452 t
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Query Match 90.5%; Score 527.6; DB 11; Length 1949;
 Best Local Similarity 94.2%; Pred. No. 2,1e-113;
 Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;


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Best Local Similarity 94.2%; Pred. No. 2.5e-113;
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 ATGGCCACCCAGCTCGGCCCGCAGACACCGGCTCTGGTGCAGACTTGTAGGTTAT 60
DB 209 ATGGCCACCCAGCTCGGCCCGCAGACACCGGCTCTGGTGCAGACTTGTAGGTTAT 268
QY 61 AAGCTGAGGAGAGAGGTTATGCTGTGAGGTTGGCCCGGAGGCGCCAGCAGCTGAC 120
DB 269 AAGCTGAGGAGAGGTTATGCTGTGAGGTTGGCCCGGAGGCGCCAGCAGCTGAC 328
QY 121 CCCTGACCAAGCCATGCGGCGAGCTGAGATGATTCGAGACCGCTTCGGGCGCAC 180
DB 329 CCCTGACCAAGCCATGCGGCGAGCTGAGATGATTCGAGACCGCTTCGGGCGCAC 388
QY 181 TTCTGTATCTGGCGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAGCTTCACC 240
DB 389 TTCTGTATCTGGCGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAGCTTCACC 448
QY 241 CAGGTTCCGACAGAACTTTTCAAGGGGCGCCAACTGGGGCGGCTTGTAGCCTTTT 300
DB 449 CAGGTTCCGACAGAACTTTTCAAGGGGCGCCAACTGGGGCGGCTTGTAGCCTTTT 508
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DB 509 GTCTTTGGGCTCAGCTGTGCTGAGAGTGTCAACAAGAGATGGAACCTTCGTGGGA 568
QY 361 CAAAGTCAGAGTGGATGTGTGGCTTACCTGGAGACCGGCTGGCTGACTGGATCCACAGC 420
DB 569 CAAAGTCAGAGTGGATGTGTGGCTTACCTGGAGACCGGCTGGCTGACTGGATCCACAGC 628
QY 421 AGTGGGGGCTGGCGGAGTTTACAGCTCTATAGGGGACGGGCGCTCGAGGAGGCGCG 480
DB 629 AGTGGGGGCTGGCGGAGTTTACAGCTCTATAGGGGACGGGCGCTCGAGGAGGCGCG 688
QY 481 CGTCTCGGGAGGGGAACCTGGGATCAGTGTAGACAGAGTCTCAGCGGGGCGCTGCACTG 540
DB 689 CGTCTCGGGAGGGGAACCTGGGATCAGTGTAGACAGAGTCTCAGCGGGGCGCTGCACTG 748

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CY 541 GGGGCCCTGTAAGTCTAGGGCCCTTTTGTGTCAGCAAGTGA 582
DB 749 GGGGCCCTGTAAGTCTAGGGCCCTTTTGTGTCAGCAAGTGA 790

RESULT 5
BY715200 969 bp mRNA linear EST 17-DEC-2002
BY715200 RIKEN full-length enriched, adult male testis Mus musculus
cDNA clone 493048d06 5', mRNA sequence.
BY715200
BY715200.1 GI:27128317
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 969)
Oxazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Miyosawa, H.,
Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,
Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A.,
Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S.,
Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani,
L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. P., Forrest,
A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,
Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J.,
Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M.,
King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons,
P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki,
H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Partea, G.,
Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D.,
Ramachandran, S., Ravasi, T., Reed, J. C., Reid, D. J., Reid, J., Ring,
B. Z., Ringwald, M., Sandelin, A., Schneider, C., Sempile, C. A., Setou,
M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale,
R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y.,
Watanabe, Y., Wells, C., Wilming, L. G., Wyszewski, B., Yanagisawa,
M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,
Carninci, P., Hayashizumi, S., Hirozane-Kishikawa, T., Konno, H., Nakamura,
M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Azawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii,
Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata,
K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander,
E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12466951
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp
URL: http://genome.gsc.riken.go.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda,
S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K.,
Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno,
H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K.,
Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y.,
Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct
Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.

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Best Local Similarity	94.0%;	Pred. No. 4.2e-113;			
Matches 547;	Conservative	0;	Mismatches 35;	Indels 0;	Gaps 0;
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QY	61	AAGCTGAGGCAGAAAGGTTATGCTGTGGAGCTGGCCGCCGGGAGGGCCCCAGACAGCTGAC	120		
Db	192	AAGCTGAGGCAGAAAGGTTATGCTGTGGAGCTGGCCCTGGGAGAGCCACCGCCGCAC	251		
QY	121	CCGCTGCACCAAGCCATCGCGGCAGCTGGAGATGAGTTCGAGACCCCGCTTCCGGCGCAC	180		
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Db	432	GTCTTTGGGGCTGGCCCTGTGTGTGTGAGAGTGTCAACAAGAAATGGAGCCCTTTGGTGGGA	491		
QY	361	CAAGTCAGAGATGGATGGTGGCCCTACTGTGAGACGGGCTGGCTGACTGATCCACAGC	420		
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QY 121 CGCTGCGCCAGGAGTGGGCGAGCTGGAGATGAGTTCGAGACCGGCTTCGGGCGAC 180
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 QY 181 TTCTCTGATCTGGCGGCTCAGCTGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 240
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 QY 241 CAGGTCTCGACGAACTTTTCAAGGGGCGCCCAACTGGGGCGGCTTGTAGCTTCCTT 300
 DB 385 CAGGTCTCGACGAACTTTTCAAGGGGCGCCCAACTGGGGCGGCTTGTAGCTTCCTT 444
 QY 301 GTCTTTGGGGCTGCACTGTG-TGCTGAGAGTGTCAACAGAGGATGGAACCACTGGTGG 359
 DB 445 GTCTTTGGGGCTGCACTGTG-TGCTGAGAGTGTCAACAGAGGATGGAACCACTGGTGG 504
 QY 360 ACAAGTGCAGGAGTGTGATGGTGGCTTACCT-GGAGACCGGCTGGCTGACTGGATCCACA 416
 DB 505 ACAAGTGCAGGAGTGTGATGGTGGCTTACCTGGAGACCGGCTGGCTGACTGGATCCACA 564
 QY 419 GCAGTGGGGCTGGGCGGAGTTCACAGCTCTATAC-GGGGACGGGGCGCTGGAGAGGCG 477
 DB 565 GCAGTGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGGACGGGGCGCTGGAGAGGCG 624
 QY 478 CGGCGTCTCGGGAGGGAGTGGGCA-TCAGTGGAGCAG-TGCTGAGGGGCGGCGTGG 535
 DB 625 CGGCGTCTCGGGAGGGAGTGGGCA-TCAGTGGAGCAG-TGCTGAGGGGCGGCGTGG 684
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RESULT 7
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 LOCUS AGENCOURT_10030867 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6491566
 DEFINITION 5', mRNA sequence.
 ACCESSION BU503850
 VERSION BU503850.1 GI:22810083
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 967)
 AUTHORS NIH-MGC <http://imgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAX14043 row: c column: 23
 High quality sequence stop: 524.
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 /clone_lib="NIH_MGC_94"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site:1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dr primed.
 Average insert size 3.3 kb. Library enriched for
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BASE COUNT 199 a 255 c 348 g 165 t
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 Query Match 80.7%; Score 470.4; DB 13; Length 967;
 Best Local Similarity 93.0%; Pred. No. 4.6e-100;
 Matches 547; Conservative 0; Mismatches 36; Indels 5; Gaps 5;
 QY 1 ATGGGACCCAGGCTCGGCCCCAGACACACAGGGCTCTGTGGCAGACTTTGTAGCTTAT 60
 DB 130 ATGGGACCCAGGCTCAACCCAGACACACAGGGCTCTGTAGCTGACTTTGTAGCTTAT 189
 QY 61 AAGCTAGGAGAGAGGTTATGCTGTGGAGCTGGCCCGGGGAGGCGCCAGCAGCTGAC 120
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 QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTTCAGAGACCCGCTTCCGCGCAC 180
 DB 250 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGGAGACCCGTTCCGCGCAC 309
 QY 181 TTCTCTGATCTGGGGCTCAGCTGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 240
 DB 310 TTCTCTGATCTGGGGCTCAGCTGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 369
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 DB 370 CAGGTCTCCGACGAACTTTTCAAGGGGCGCCCAACTGGGGCGGCTTGTAGCTTCCTT 429
 QY 301 GTCTTTGGGGCTGCACITGCTGTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
 DB 430 GTCTTTGGGGCTGCCCTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 489
 QY 361 CAAGTCAGAGTGGATGCTGGGCTA-CCTGAGAGCGGCTGGCTGACTGGATCCACAG 419
 DB 490 CAAGTCAGAGTGGATGCTGGGCTA-CCTGAGAGCGGCTGGCTGACTGGATCCACAG 549
 QY 420 CAGT-GGGGGCTGGGGAGTTCACAGCTCTATACGGGAC-GGGGCCCTGGAGGAGCG 477
 DB 550 CAGTGGGGGCTGGGGAGTTCACAGCTCTATACGGGACGGGGGCGCTGGAGGAGGCA 609
 QY 478 CGGCGTCTGGGGAGGGGAACTGGGCATCAGTGAGACAGTGTGAC-GGGGGCGCTGGC 536
 DB 610 CGGCGTCTGGGGAGGGGAACTGGGCATCAGTGAGACAGTGTGACGGGGGCGCTGGC 669
 QY 537 ACTGGGGCGCTGTAACTGT-AGGGGCCCTTTTGTAGCAAGTGAA 583
 DB 670 ACTGGGGCGCTGT-ACCTGTAAAGGGGCCCTTTTGTAGCAAGTGGA 717
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 CA391923 626 bp mRNA linear EST 06-NOV-2002
 LOCUS CS20C09.y1 Human Retinal pigment epithelium/choroid cDNA
 DEFINITION (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs20c09
 5', mRNA sequence.
 ACCESSION CA391923
 VERSION CA391923.1 GI:24724221
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 626)
 AUTHORS Wistow, G., Bernstein, S.L., Wyatt, M.K., Farris, R.N., Behal, A.,
 Touchman, J.W., Bouffard, G., Smith, D., and Peterson, K.
 TITLE Expressed sequence tag analysis of human RPE/choroid for the
 NEIBank Project: Over 6000 non-redundant transcripts, novel genes
 and splice variants
 JOURNAL Mol. Vis. 8 (4), 205-220 (2002)
 MEDLINE 22103460
 PUBMED 12107410
 COMMENT Contact: Wistow G
 Section on Molecular Structure and Function

National Eye Institute
6/331, N.H., Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 20 row: c column: 09
Seq primer: M13R1 reverse primer (ABI).

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cs20c09"
/tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Retinal pigment epithelium/choroid cDNA
(Un-normalized, unamplified): cs"
/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor
eyes (75-80 years old) yielded approximately 600 mg of
dissected RPE/choroid tissue. This in turn yielded 340 ug
of total RNA and 7 ug of mRNA. A directionally cloned cDNA
library in the pCMVSPORT6 vector was constructed at Life
Technologies (Rockville, MD; now part of Invitrogen Corp),
essentially following the protocols of the SuperScript
Plasmid System (Invitrogen Corp).
<http://www.invitrogen.com/>). The library code
designated was cs. For this library, cDNA inserts were
cloned into the NotI/MluI sites of the vector. EST
analysis was performed on the unamplified library at the
NIH Intramural Sequencing Center (NISC)."
BASE COUNT 108 a 202 c 197 g 118 t
ORIGIN

Query Match 76.8%; Score 447.8; DB 14; Length 626;
Best Local Similarity 99.3%; Pred. No. 8.2e-95;
Matches 449; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGGGACCCAGGCTCGGCCCCACACACAGGGCTCTGGTGGAGACTTTGTAGGTTAT 60
DB 175 ATGGGACCCAGGCTCGGCCCCACACACAGGGCTCTGGTGGAGACTTTGTAGGTTAT 234
QY 61 AAGCTGAGCGAGAGGGTTATGTCGTGAGCTGGCCCGGGAGGCCACAGACTGAC 120
DB 235 AAGCTGAGCGAGAGGGTTATGTCGTGAGCTGGCCCGGGAGGCCACAGACTGAC 294
QY 121 CCGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTTCGAGACCCGCTTCGGCGCACC 180
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QY 181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGGCCAGCAACGGTTTCAAC 240
DB 355 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGGCCAGCAACGGTTTCAAC 414
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QY 301 GTCTTTGGGGTGCACCTGTGTGCTGAGAGTGTCAACAGGAGATGGAAACCACTGGTGGGA 360
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QY 361 CAAAGTGCAAGAGTGTGATGGTGGCTTACTGTGAGAGCGGGCTGGCTGATGATGCACAGC 420
DB 535 CAAAGTGCAAGAGTGTGATGGTGGCTTACTGTGAGAGCGGGCTGGCTGATGATGCACAGC 594
QY 421 AGTGGGGCTGGCGGAGTTCACACCTCTATA 452
DB 595 AGTGGGGCTGGCGGAGTTCACACCTCTATA 626

RESULT 9
B1910270

LOCUS B1910270 643 bp mRNA linear EST 16-OCT-2001
DEFINITION 603069493F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218294 5',
rRNA sequence.
ACCESSION B1910270
VERSION B1910270.1 GI:16173653
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 643)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11548 row: j column: 23
High quality sequence stop: 643.

FEATURES

Location/Qualifiers
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/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH MGC 118"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH MGC Library."
BASE COUNT 129 a 184 c 216 g 114 t
ORIGIN

Query Match 72.5%; Score 422.4; DB 12; Length 643;
Best Local Similarity 94.3%; Pred. No. 7.5e-89;
Matches 449; Conservative 0; Mismatches 26; Indels 1; Gaps 1;
QY 1 ATGGGACCCAGGCTCGGCCCCACACACAGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
DB 140 ATGGGACCCAGGCTCGGCCCCACACACAGGGCTCTGGTGGCAGACTTTGTAGGTTAT 199
QY 61 AAGCTGAGCGAGAGGGTTATGTCGTGAGCTGGCCCGGGAGGCCACAGACTGAC 120
DB 200 AAGCTGAGCGAGAGGGTTATGTCGTGAGCTGGCCCGGGAGGCCACAGACTGAC 259
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DB 260 CCGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTTCGAGACCCGCTTCGGCGCACC 319
QY 181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGGCCAGCAACGGTTTCAAC 240
DB 320 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGGCCAGCAACGGTTTCAAC 379
QY 241 CAGGTCTCCGAGCACTTTTCAAGGGGGCCCCAACTGGGGCCGCTTGTAGCCTTCTTT 300
DB 380 CAGGTCTCCGAGCACTTTTCAAGGGGGCCCCAACTGGGGCCGCTTGTAGCCTTCTTT 439
QY 301 GTCTTTGGGGTGCACCTGTGTGCTGAGAGTGTCAACAGGAG-ATGGAACCACTGGTGGG 359
DB 440 GTCTTTGGGGTGCACCTGTGTGCTGAGAGTGTCAACAGGAGATGGAACCACTGGTGGG 499

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QY 360 ACAAGTGCAGAGTGGATGGTGGCCCTACCTGGAGACGGCGCTGGCTGACTGATCCACAG 419
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QY 420 CAGTGGGGCTGGCGGAGTTCACAGCTCTATACGGGACGGGGCCCTGGAGAGG 475
DB 560 CAGTGGGGCTGGCGGAGTTCACAGCTCTATACGGGACGGGGCCCTGGAGAGG 515

RESULT 10
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LOCUS 602111728F1 NC1_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4239798
DEFINITION 5', mRNA sequence.
ACCESSION BF785386
VERSION BF785386.1 GI:12090422
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1. (bases 1 to 815)
AUTHORS N.H.-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-f@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9853 row: h column: 07
High quality sequence start: 3
High quality sequence stop: 650.

FEATURES
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/strain="FVB/N"
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/clone_lib="NCI CGAP Kid14"
/notes="Organ: kidney; Vector: pCMV-SpORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NC-CGAP Library. |"
BASE COUNT 166 a 212 c 296 g 141 t
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Query Match 68.6%; Score 400.2; DB 10; Length 815;
Best Local Similarity 91.4%; Pred. No. 1.3e-63;
Matches 502; Conservative 0; Mismatches 38; Indels 9; Gaps 7;

QY 21 CCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGTTATTAAGCTAGGAGGAGGTTA 80
DB 2 CCCAGACACACGGGCTCTAGTGGTTGAC-TTGTAGGCTATAAGCTAGGAGGAGGTTA 60
QY 81 TGTCTGTGGAGCTGGCCCGGGAGGGCCAGACAGTGCACCCCTGCACAGCCATGG 140
DB 61 TGTCTGTGGAGCTGGCCCGGGAGGGCCAGACAGTGCACCCCTGCACAGCCATGG 120
QY 141 GGACGTGGAGATGAGTTTCAGACACCCGCTTCGGCGCACCTTCTGTGATCTGCGGCTCA 200
DB 121 GGCTGTGGAGACAGATT-GAGACCCGCTTCGCGGCACCTTCTGTGACTGCGGCTCA 179
QY 201 GCTGCATGTGACCCCGAGGCTCAGCCCAACAGCTTTCACCCAGGCTTCGACGAACTTT 260
DB 180 GCTACAGTGCACCCCGAGGCTCAGCCCAACAGCTTTCACCCAGGTTTCGACGAACTTT 239

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QY 261 TCAAGGGGGCCCCCACTGGGGCGCCCTTGTAGCCTTCTTTTGTCTTTTGGGCTGCATGTG 320
DB 240 CCAAGGGGGGGCCCTAACTGGGGCGCCCTTGTGGCACTTCT--TGTCTTTGGGCTGCCTGTG 296
QY 321 TGTGACAGTGTCAACAAGGAGATGGAACCACTGGTGGGACAAAGTGACAGAGTGGATGGT 380
DB 297 TGTGACAGTGTCAACAAGAAATGGAGCC-TTGGTGGGACAAAGTGACAGATTTGGATGGT 355
QY 381 GGCCTACTTGGAGACGGCGCTGCTGACTGATCCACAGCAGTGGGGGCTGSGCGGAGTT 442
DB 356 GGCCTACTTGGAGACAGCTCTGGCTGACTGCATCCACAGCAGTGGGGGCTGSGCGGAGTT 415
QY 441 CACAGCTCTATACGGGACCGGGCCCTGGAGGAGCGCGCTCTCGGAGAGGGGAACTG 500
DB 416 CACAGCTCTATACGGGACCGGGCCCTGGAGGAGCGCACGG-GTCTGCGGAGGGGAAAC-G 473
QY 501 GGCATCAGTGAAGGACAGTGTGACGGGGCGCTGGGCACCTGGGGGCTTGAAGTGTAGG 560
DB 474 GGCATCAGTGAAGGACAGTGTGACGGGGCGCTGGGCACCT-GGGGCGCTTGAAGTGTAGG 532
QY 561 GGCCTTTT 569
DB 533 GGCCTTTT 541

RESULT 11
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LOCUS AMGNNUC:NRDGI-00100-H10-A nrdgi (10855) Rattus norvegicus cDNA
DEFINITION clone nrdgi-00100-h10 5', mRNA sequence.
ACCESSION CBS78463
VERSION CBS78463.1 GI:29522504
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1. (bases 1 to 623)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00100 row: h column: 10.
Location/Qualifiers
source 1. .623
/organism="Rattus norvegicus"
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/db_xref="taxon:10116"
/clone="nrdgi-00100-h10"
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/clone_lib="nrdgi (10855)"
/notes="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; rat
dorsal root ganglia"
BASE COUNT 114 a 207 c 184 g 118 t
ORIGIN
Query Match 66.3%; Score 386.6; DB 14; Length 623;
Best Local Similarity 93.3%; Pred. No. 1.9e-80;
Matches 404; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGAGGCTCGGGCCCGCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
DB 191 ATGGCGACCCCGAGGCTCAACCCCGACACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 250
QY 61 AAGCTGAGGCGAAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCGACAGCTGAC 120
DB 251 AAGCTGAGGCGAAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCGACAGCTGAC 310

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(MGI:MGI:108052)

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ANRAAGDEFTFRFTFSDLAAGHVTGSAQCFYDSBELFQGGPNWGLVAFVVF
GAALCAESYKMEPLVQVDMVAYILETRLDWIHSSGGWVRSSQLLSAS-YKVG
LHKIGPLMGWGCAGRG"
BASE COUNT 178 a 229 c 264 g 183 t
ORIGIN

Query Match 65.2%; Score 380.2; DB 11; Length 854;
Best Local Similarity 92.4%; Pred. No. 6.5e-79;
Matches 400; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 1 ATGGCGACCCAGCCCTGGCCCGCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
196 ATGGCGACCCAGCCCTAAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 255
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 AAGCTGAGCGAAGAGGTTATGCTGTGGAGCTGGCCCGGAGGCGCCAGCAGCTGAC 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
256 AAGCTGAGCGAAGAGGTTATGCTGTGGAGCTGGCCCGTGGGGAAGGCCAGCGCCGAC 315
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 CGCTGACCAAGCACTGGCGGAGCTGAGATGATGTCGAGACCGGCTTCGGGGCACC 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
316 CGCTGACCAAGCACTGGCGGAGCTGTCGAGACGAGTTTGTAGACCGGTTTCGGCGCACC 375
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAGCAAGCTTCACC 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
376 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAGCAAGCTTCACC 435
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241 CAGGTTCCGACGAACTTTTCAAGGGGCGCCAACTGGGGCGCGCTTGTAGCCTTCTTT 300
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436 CAGGTTCCGACGAACTTTTCAAGGGGCGCCAACTGGGGCGCGCTTGTAGCCTTCTTT 495
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301 GTCTTTGGGGCTGACTGTGCTGAGAGTGTCACAGAGAGATGGAACCACTGGTGGGA 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
496 GTCTTTGGGGCTGCGCTGTGCTGAGAGTGTCACAAAGAAATGGAGCCCTTTGGTGGGA 555
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 CAAGTGACGAGTGGATGTGCTACCTGAGAGACGCGCTGCTGACTGGATCCACAGC 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
556 CAAGTGACGAGTGGATGTGCTGAGAGACGCTGAGAGACGCTGCTGCTGAGTCCACAGC 615
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 AGTGGGGCTGGG 433
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
616 AGTGGGGCTGGG 628

RESULT 13
BG298789 792 bp mRNA linear EST 21-FEB-2001
LOCUS 602396527F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4511215 5',
DEFINITION mRNA sequence.
ACCESSION BG298789
VERSION BG298789.1 GI:13063794
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 792)
NIH-MGC <http://mgi.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
P-ate: LLAM10394 row: e column: 08
High quality sequence stop: 713.
FEATURES
Location/Qualifiers
Source 1..792
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:4511215"
/tissue_type="retina"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC_94"
/notes="Organ: eye; Vector: pCMV-SPORT6; Site: 1; NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."
BASE COUNT 174 a 201 c 246 g 171 t
ORIGIN

Query Match 63.3%; Score 369; DB 10; Length 792;
Best Local Similarity 91.8%; Pred. No. 2.7e-76;
Matches 401; Conservative 0; Mismatches 35; Indels 1; Gaps 2;
QY 1 ATGGCGACCCAGCCCTGGCCCGCAGACACACGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
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61 AAGCTGAGCGAAGAGGTTATGCTGTGGAGCTGGCCCGGAGGCGCCAGCAGCTGAC 120
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159 AAGCTGAGCGAAGAGGTTATGCTGTGGAGCTGGCCCGTGGGGAAGGCCAGCGCCGAC 218
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121 CCGCTGACCAAGCACTTTTCAAGGGGCGCCAACTGGAGACCGGCTTCCGCGCACC 180
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219 CCGCTGACCAAGCACTGGGGCTGTGGAGACGAGTTTGAGACCGGCTTTCGCGCGCACC 278
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279 TTCTCTGACCTGGC-GCTCAGCTACACGTCACGCCAGGCTCAGCCAGCAACGCTTCACC 337
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301 GTCTTTGGGGCTGACTGTGCTGAGAGTGTCACCAAGAGATGGAACCACTGGTGGGA 360
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398 GTCTTTGGGGCTGCGCTGTGCTGAGAGTGTCACCAAGAAATGGAGCCCTTGGTGGGA 457
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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458 CAAAGTGAGAGTGGATGTGCTACCTGAGAGACGCTGCTGCTGACTGGATCCACAGC 517
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 AGTGGGGCTGGGCGGA 437
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518 AGTGGGGCTGGTAA 534

RESULT 14
CA407899 548 bp mRNA linear EST 07-NOV-2002
LOCUS 1004048 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens
DEFINITION cDNA 5', mRNA sequence.
ACCESSION CA407899
VERSION CA407899.1 GI:24772770
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 548)
Yang R.-Z., Shuldiner, A. and Gong, D.-W.
AUTHORS
TITLE EST analysis of human adipose gene expression

JOURNAL COMMENT

Unpublished

Contact: Gong Da-Wei
Division of Endocrinology, Diabetes and Nutrition
University of Maryland
660 Redwood St., H4497, Baltimore, MD 21201, USA
Tel: 410 706 1672
Fax: 410 706 1622
Email: dgong@medicine.umaryland.edu
PCR Primers
FORWARD: CTCGGGAAGCGGCCAATTGCTGTGGT
BACKWARD: AATACGACTCACTATAGGGGAATTGG
Seq primer: GTTGTACCGGATTC.

FEATURES

source

Location/Qualifiers
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/sex="Male and Female"
/tissue_type="Adipose"
/clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
/note="Vector: lambdaTriplex"
BASE COUNT: 109 a 148 c 182 g 169 t
ORIGIN

Query Match 62.6%; Score 364.8; DB 14; Length 548;
Best Local Similarity 99.2%; Pred. No. 2.4e-75;
Matches 377; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 174 GGCACCTTCTCTGATCTGGGGCTCAGCTGATGACCCAGGCTCAGCCAGCAACG 233
DB 1 GGCACCTTCTCTGATCTGGGGCTCAGCTGATGACCCAGGCTCAGCCAGCAACG 60
QY 234 CTTACCCAGGTCTCCGACGAACTTTTCAAGGGGGCCCCAAGCTGGGCGCCCTGTAGC 293
DB 61 CTTACCCAGGTCTCCGATGAACCTTTTCAAGGGGGCCCCAAGCTGGGCGCCCTGTAGC 120
QY 294 CTTCTTCTCTTTGGGGTGCACCTGTGTCTGAGAGT-GTCAACAAGGAGATGAACCC 352
DB 121 CTTCTTCTCTTTGGGGTGCACCTGTGTCTGAGAGTGTCAACAAGGAGATGAACCC 180
QY 353 TGGTGGGCAAGTCAGGAGTGGATGGTGGCTACCTCGACAGCGGCTGGCTGACTGGA 412
DB 181 TGGTGGGCAAGTCAGGAGTGGATGGTGGCTACCTCGACAGCGGCTGGCTGACTGGA 240
QY 413 TCCACAGCAGTGGGGCTGGCGGAGTTTACAGCTCTATA-GGGGACGCGGCCCTGAGG 472
DB 241 TCCACAGCAGTGGGGCTGGCGGAGTTTACAGCTCTATA-GGGGACGCGGCCCTGAGG 300
QY 473 AGGCGCGGCTCTGGGAGGGGAACTGGGCATCAGTCAGGACAGTGTGACGGGGCGG 532
DB 301 AGGCGCGGCTCTGGGAGGGGAACTGGGCATCAGTCAGGACAGTGTGACGGGGCGG 360
QY 533 TGGCACTGGGCGCCCTGGTA 552
DB 361 TGGCACTGGGCGCCCTGGTA 380

RESULT 15

BU557268

LOCUS

AGENCY 10253293 NIH MGC 109 Homo sapiens linear EST 16-SEP-2002

DEFINITION

IMAGE:6585108 5', mRNA sequence.

ACCESSION

BU557268

VERSION

BU557268.1 GI:22907564

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 869)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLC2796 row: i column: 12
High quality sequence stop: 603.

FEATURES

source

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6585108"
/tissue_type="teratocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 109"
/notes="Organ: ovary; Vector: pOTS7; Site 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G) Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 157 a 219 c 310 g 182 t 1 others
ORIGIN

Query Match 62.4%; Score 363.8; DB 13; Length 869;
Best Local Similarity 99.5%; Pred. No. 4.6e-75;
Matches 365; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 217 GGCCTAGCCAGCAACGCTTACCCAGGCTCCGACGAACCTTTTCAAGGGGGCCCCAAC 276
DB 2 GGCCTAGCCAGCAACGCTTACCCAGGCTCCGACGAACCTTTTCAAGGGGGCCCCAAC 60
QY 277 TGGGGCGGCTTGTAGCCTTTTGTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAAC 336
DB 61 TGGGGCGGCTTGTAGCCTTTTGTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAAC 120
QY 337 AAGGAGATGGAACCACTGTGGACAAAGTCAGGAGTGGATGGTGGCCCTACCTGGAGACG 396
DB 121 AAGGAGATGGAACCACTGTGGACAAAGTCAGGAGTGGATGGTGGCCCTACCTGGAGACG 180
QY 397 CGCTGGCTGACTGGATCCACAGCAGTGGGGGCTGGCGGAGTTACAGCTCTATACGGG 456
DB 181 CGCTGGCTGACTGGATCCACAGCAGTGGGGGCTGGCGGAGTTACAGCTCTATACGGG 240
QY 457 GACGGGGCCCTGGAGAGCGCGGCGCTCTCGGGAGGGGAACTGGGCATCAGTAGGACA 516
DB 241 GACGGGGCCCTGGAGAGCGCGGCGCTCTCGGGAGGGGAACTGGGCATCAGTAGGACA 300
QY 517 GTGCTGACGGGGCGCGTGGCAGCTGGGGGCCCTGGTAACCTGTAGGGGCCCTTTTGTAGC 576
DB 301 GTGCTGACGGGGCGCGTGGCAGCTGGGGGCCCTGGTAACCTGTAGGGGCCCTTTTGTAGC 360
QY 577 AAGTGAA 583
DB 361 AAGTGAA 367

Search completed: October 27, 2003, 13:50:44
Job time : 1475.26 secs

GenCore version 5.1.6
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OM nuclicic - nucleic search, using sw model

Run on: October 27, 2003, 11:03:45 ; Search time 1735.01 Seconds
(without alignments)
13722.924 Million cell updates/sec

Title: US-09-925-674A-8

Perfect score: 582
Sequence: 1 atggcagcccccagctcaaac.....ccttttttctagcaagtea 582

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.:

- 1: gb_ba.*
- 2: gb_hcg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_p.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vt.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vt.*
- 30: em_htg_hum.*
- 31: em_htg_in.*
- 32: em_htg_oth.*
- 33: em_htg_mu.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mu.*
- 41: em_htgo_oth.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match %	Length	DB ID	Description
1	578.8	99.5	582	10 MMU59746	US9746 Mus muscu
2	578.8	99.5	3476	10 AF030769	AF030769 Mus muscu
3	563.4	96.8	581	6 AX022531	AX022531 Sequence
4	563.4	96.8	581	6 AX030819	AX030819 Sequence
5	562.8	96.7	582	10 AF096291	AF096291 Rattus no
6	562.8	96.7	3473	10 AY170344	AY170344 Mus muscu
7	558.2	95.9	579	6 AR020779	AR020779 Sequence
8	524.4	90.1	582	6 AX481423	AX481423 Sequence
9	524.4	90.1	582	9 HSU59747	U59747 Human Bcl-w
10	521.2	89.6	3542	9 D87461	D87461 Human mRNA
11	519.6	89.3	583	6 AX022529	AX022529 Sequence
12	519.6	89.3	583	6 AX030817	AX030817 Sequence
13	519.6	89.3	1437	9 BC021198	BC021198 Homo sapi
14	515	88.5	579	6 AR020780	AR020780 Sequence
15	468.4	80.5	220818	2 AC128940	AC128940 Rattus no
16	468.4	80.5	223933	2 AC097389	AC097389 Rattus no
17	429.8	73.8	3815	10 BC040369	BC040369 Mus muscu
18	429.8	73.8	237561	10 AC115591	AC115591 Mus muscu
19	415.4	71.4	210784	2 AC119293	AC119293 Rattus no
20	415.4	71.4	263901	2 AC115371	AC115371 Rattus no
21	405.6	69.7	148278	2 AC079885	AC079885 Rattus no
22	405.6	69.7	180665	2 AC084240	AC084240 Rattus no
23	405.6	69.7	221557	2 AC134055	AC134055 Rattus no
24	372.8	64.1	1098	6 BD078624	BD078624 Human pro
25	372.2	64.0	196292	9 CNS0000B	AL049823 Human chr
26	241.2	41.4	749	5 XLR1	X82462 X. laevis R1
27	218.6	37.6	6049	6 AX345130	AX345130 Sequence
28	192.6	33.1	6049	6 AX345131	AX345131 Sequence
29	142.4	24.5	1252	4 AB073983	AB073983 Canis fam
30	140.8	24.2	702	4 AY005131	AY005131 Oryctolag
31	140.8	24.2	1163	4 AB080951	AB080951 Felis cat
32	139.2	23.9	766	4 AF164517	AF164517 Ovis arie
33	136	23.6	541	4 AF245488	AF245488 Bos tauru
34	136	23.4	541	4 AF245487	AF245487 Bos tauru
35	136	23.4	541	4 AF245489	AF245489 Bos tauru
36	135	23.2	764	10 RNU10579	U10579 Rattus norv
37	135	23.2	1742	6 BD012974	BD012974 A mutagen
38	135	23.2	1742	6 BD013799	BD013799 Modified
39	135	23.2	1742	10 RNU72350	J72350 Rattus norv
40	135	23.2	2332	10 RNCBLKLS	X82537 R. norvegicu
41	134.6	23.1	636	6 BD097037	BD097037 A BH4 fus
42	134.6	23.1	702	6 BD084108	BD084108 Method of
43	134.6	23.1	702	6 BD102202	BD102202 Method fo
44	134.6	23.1	702	9 BT007208	BT007208 Homo sapi
45	134.6	23.1	702	12 BT008248	BT008248 Synthetic

ALIGNMENTS

RESULT :
MMU59746
LOCUS: MMU59746 582 bp mRNA linear ROD 29-SEP-1996
DEFINITION: Mus musculus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION: U59746
VERSION: U59746.1 GI:1572494
KEYWORDS: Mus musculus (house mouse)
SOURCE: Mus musculus
ORGANISM: Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 582)
AUTHORS: Gibson,L., Holmgren,S.P., Huang,D.C., Bernard,O., Cope, and N.G.,
Cenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
bcl-w, a novel member of the bcl-2 family, promotes cell survival

JOURNAL Oncogene 13 (4), 665-675 (1996)
MEDLINE 96358615
PUBMED 8761287
REFERENCE 2 (bases 1 to 582)
AUTHORS Gibson, J., Holmgren, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and Cory, S.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:10090"
/chromosome="14"
/cell_line="BaF3"
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/gene="bcl-w"
CDS 1..582
/gene="bcl-w"
/note="promotes cell survival; Bcl-2 homolog"
/codon_start=1
/product="Bcl-w"
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/db_xref="GI:1572495"
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BASE COUNT 107 a 158 c 200 g 117 t
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Query Match 99.5%; Score 578.8; DB 10; Length 582;
Best Local Similarity 99.7%; Pred. No. 2.7e-128;
Matches 580; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 241 CAGGTTTCCGACGAACCTTTCCAGGGGGGCCCTAACTGAGGGGGCCGCTCTGTGGCATCTTT 300
QY 301 GTCTTTGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATPGAGCCCTTTGGTGGGA 360
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QY 361 CAAGTGAGAGATTGGATGGTGGCTACTCGAGACAGTCTGGCTACTGGATCCACAGC 420
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QY 421 AGTGGCGGCTGGCGGAGTGTACAGCTCTATACGGGACCGGGCCCTGGAGAGGACACGG 480
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QY 541 GGGGCCCTGGTAACCTGTAGGGGCCCTTTTCTAGCAAGTGA 582
Db 541 GGGGCCCTGGTAACCTGTAGGGGCCCTTTTCTAGCAAGTGA 582
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AF030769 3476 bp mRNA linear ROD 16-NOV-1997
LOCUS Mus musculus BCL-W (Bcl-w) mRNA, complete cds.
DEFINITION AF030769
ACCESSION AF030769
VERSION AF030769.1 GI:2623249
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3476)
AUTHORS Ross, A.J., Waymire, K.G., Moss, J.E., Parlow, A.F., Russell, L.D. and MacGregor, G.R.
TITLE Bcl-w is required for testis homeostasis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3476)
AUTHORS Ross, A.J. and MacGregor, G.R.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-1997) Center for Molecular Medicine, Emory University, 1462 Clifton Road, Atlanta, GA 30322, USA
FEATURES Location/Qualifiers
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BASE COUNT 796 a 814 c 991 g 875 t
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Query Match 99.5%; Score 578.8; DB 10; Length 3476;
Best Local Similarity 99.7%; Pred. No. 2.1e-128;
Matches 580; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCGAGCCGAGCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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QY 61 AGGCTGAGGCGAAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCGCGCGAC 120
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QY 541 GGGGCCCTGTTAACTGTAGGGGCCCTTTTGTCTAGCAAGTGA 582
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RESULT 3
AX022531
LOCUS AX022531 581 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 8 from Patent EP0932674.
ACCESSION AX022531
VERSION AX022531.1 GI:10046127
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Adams,J.M., Holmgren,S.P., Cory,S. and Gibson,L.M.
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
JOURNAL Patent: EP 0932674-A 8 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)

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BASE COUNT 105 a 164 c 195 g 117 t

Query Match 96.8%; Score 563.4; DB 6; Length 581;
Best Local Similarity 98.1%; Pred. No. 1.3e-124;

Matches 570; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1 ATGGGACCCAGCCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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QY 61 AGGCTGAGGCGAAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCGCGCGAC 120
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Db 121 CCGCTGCAACCAAGCCATGGGGCTCTGGAGACGAGTTTGAGACCGCTTCCCGCGCACC 180
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QY 421 AGTGGCGCTGGCGGAGTTCACAGCTCTATACGGGACCGGGCCCTGGAGGAGGACCG 480
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QY 541 GGGGCCCTGTTAACTGTAGGGGCCCTTTTGTCTAGCAAGTGA 581
Db 541 GGGGCCCTGTTAACTGTAGGGGCCCTTTTGTCTAGCAAGTGA 581

RESULT 4
AX030819
LOCUS AX030819 581 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 8 from Patent WO9735971.
ACCESSION AX030819
VERSION AX030819.1 GI:10278313
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Adams,J.M., Holmgren,S.P., Cory,S. and Gibson,L.M.
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
JOURNAL Patent: WO 9735971-A 8 02-OCT-1997;
ADAMS JERRY MCKEE (AU); HOLMGREN SHAUN P (AU); CORY SUZANNE (AU)
; GIBSON LEONIE M (AU); AMRAD OPERATIONS PTY LTD (AU)

FEATURES
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RLREGNWA"
BASE COUNT 105 a 164 c 195 g 117 t

Query Match 96.8%; Score 563.4; DB 6; Length 581;
Best Local Similarity 98.1%; Pred. No. 1.3e-124;

[illegible]

ACCESSION AV170344
 VERSION AV170344.1 GI:27497698
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Mus.
 REFERENCE 1 (bases 1 to 3473);
 Su,H.-Y.
 Extraction from neonatal mouse skin after iGF-1 stimulation:
 TITLE Unpublished
 JOURNAL
 REFERENCE 2 (bases 1 to 3473);
 Su,H.-Y.
 Direct Submission
 TITLE Submitted (29-OCT-2002) Biotechnology, Pingtung University, No. 1,
 JOURNAL Heueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan
 LOCATION/Qualifiers
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 BASE COUNT 758 a 831 c 1021 g 863 t
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 Query Match 96.7%; Score 562.8; DB 10; Length 3473;
 Best Local Similarity 97.9%; Pred. No. 1.5e-124;
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 QY 1 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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QY 461 CCTCTGGGGAGGGAACTGGGCATCAGTGAGGACAGTCTGCTACCGGGGGCCCTGGCACTG 540
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 RESUIT 7
 AR020779
 LOCUS AR020779 579 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 1 from patent US 5789201.
 ACCESSION AR020779
 VERSION AR020779.1 GI:3975394
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 1. (bases 1 to 579)
 AUTHORS Guastella,J.
 TITLE Genes coding for bcl-1 and bcl-2 homologues
 JOURNAL Patent: US 5789201-A; 04-AUG-1998;
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 Best Local Similarity 97.8%; Pred. No. 2.4e-123;
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RESULT 8
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LOCUS      AX481423      582 bp      DNA      linear      PAT 16-AUG-2002
DEFINITION Sequence 37 from Patent WO02055693.
ACCESSION  AX481423
VERSION     AX481423.1  GI:22316337
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Kneutzer,R., Limmer,S., Rost,S. and Hadwiger,P.
TITLE      Method for inhibiting the expression of a target gene
JOURNAL    Patent: WO 02055693-A 37 18-JUL-2002;
            Ribopharma AG (DE)
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BASE COUNT 104 a 156 c 211 g 111 t
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Best Local Similarity 93.8%; Pred. No. 3e-115;
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DB 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAGATGGAACCACTGGTGGGA 360
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LOCUS      HSU59747      582 bp      mRNA      linear      PRI 29-SEP-1996
DEFINITION Human Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION  U59747
VERSION     U59747.1  GI:1572492
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 582)
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Gibson,L., Holmgren,S.P., Huang,D.C., Bernard,O., Copeland,N.G.,
            Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
            bcl-w, a novel member of the bcl-2 family, promotes cell survival
            Oncogene 13 (4), 665-675 (1996)
            8761287
            PUBMED
            96358615
            MEDLINE
            2 (bases 1 to 582)
            Gibson,L., Holmgren,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and
            Cory,S.
            Direct Submission
            Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
            Eliza Hall Institute of Medical Research, PO Royal Melbourne
            Hospital, Parkville, Victoria 3050, Australia
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BASE COUNT 104 a 156 c 211 g 111 t
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Query Match: 90.1%; Score 524.4; DB 9; Length 582;
Best Local Similarity 93.8%; Pred. No. 3e-115;
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QY 541 GGGGCGCTGGTAACTGTAGGGGCGCTTTTCTGCTAGCAAGTGA 582
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RESULT 10
LOCUS D87461 3542 bp mRNA linear PRI 06-OCT-2003
DEFINITION Human mRNA for KIAA0271 gene, complete cds.
ACCESSION D87461
VERSION D87461.1 GI:1944417
KEYWORDS KIAA0271.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayashi,Y.,
Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.
TITLE Prediction of the coding sequences of unidentified human genes. V2.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
analysis of cDNA clones from cell line KG-1 and brain
DNA Res. 3 (5), 321-329 (1996)
JOURNAL 97191544
MEDLINE 9039502
PUBMED
REFERENCE 2 (bases 1 to 3542)
AUTHORS Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute;
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:cdna@infoakusa.or.jp, Tel:+81-438-52-3913)
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BASE COUNT 804 a 817 c 1030 g 891 t
Query Match 89.6%; Score 521.2; DB 9; Length 3542;
Best Local Similarity 93.5%; Pred. No. 1.4e-114;

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Matches 544; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 1 ATGGGACCCCAAGCCTCAACCCGACACACACGGGCTCTAGTGGCTGACTTTAGGCTAT 60
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RESULT 11
LOCUS AX022529 583 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 6 from Patent EP0932674.
ACCESSION AX022529
VERSION AX022529.1 GI:10046125
KEYWORDS
SOURCE
ORGANISM
unidentified
unidentified
unclassified.
REFERENCE 1
AUTHORS Adams,J.M., Holmgren,S.P., Cory,S. and Gibson,L.M.
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
JOURNAL Patent: EP 0932674-A 6 04-AUG-1999;
AVRAD OPERATIONS PTY LTD (AU)
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Query Match      89.3%; Score 519.6; DB 6; Length 583;
Best Local Similarity 93.3%; Pred. No. 4.3e-114;
Matches 543; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
1 ATGGCGACCCCGAGCTCAACCCAGACACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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QY 541 GGGGCCCTGTAACTGTAGGGCCCTTTTGTGCTAGCAAGTGA 582
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LOCUS      1437 bp      mRNA      linear      PRI 22-JAN-2002
DEFINITION Homo sapiens, BCL2-like 2, clone MGC:10675 IMAGE:3944307, mRNA,
complete cds.
ACCESSION BC021198
VERSION    BC021198.1 GI:18203706
KEYWORDS   MGC.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 1437)
AUTHORS   Strausberg R.
TITLE     Direct Submission
JOURNAL   Submitted (14-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

BASE COUNT      105 a   157 c   210 g   111 t
ORIGIN
Query Match      89.3%; Score 519.6; DB 6; Length 583;
Best Local Similarity 93.3%; Pred. No. 4.3e-114;
Matches 543; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
1 ATGGCGACCCCGAGCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db 1 ATGGCGACCCCGAGCTCGGCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
QY 61 AGCTGAGCAGAGAGGGTTATGCTGTGAGAGTGGCCCTGGGAAAGGCCAGCCGCCAC 120
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RESULT 12
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LOCUS      583 bp      DNA      linear      PAT 20-SEP-2000
DEFINITION Sequence 6 from Patent WO9735971.
ACCESSION AX030817
VERSION    AX030817.1 GI:10278311
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified.
REFERENCE  1
AUTHORS   Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M.
TITLE     A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
JOURNAL   Patent: WO 9735971-A 6 02-OCT-1997;
ADAMS JERRY MCKEE (AU); HOLMGREEN SHAUN P (AU); CORY SUZANNE (AU);
; GIBSON LEONIE M (AU); AMRAD OPERATIONS PTY LTD (AU)
LOCATION/Qualifiers
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CDS
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REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.mci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DP
 cDNA Library Preparation: Rubin laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mc@nigri.nih.gov
 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Ho, S.-L., Legaspi, R.,
 Lim, M., Maduro, Q.L., Masello, C., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Snyder, B., Startipop, S., Thomas, P.J.,
 Tingson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.I., Walker, M.A.,
 Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 15 Row: k Column: 19
 This clone was selected for full length sequencing because it
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Query Match 89.3%; Score 519.6; DB 9; Length 1437;
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 QY 1 ATGGGACCCAGCCTCAACCCAGACACACACGGGCTCTAGTGGCTGATTTGTAGGCTAT 60
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 DB 296 CCACTGCACCAAGCCATGCGGCGAGTGGAGATGAGTTGACACCCGCTTCGGCGCAC 355
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 DEFINITION Sequence 2 from patent US 5789201.
 ACCESSION AR020780
 VERSION AR020780.1 G:3975395
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 579)
 AUTHORS Guastella, J.
 TITLE Genes coding for bcl-2 homologues
 JOURNAL Patent: US 5789201-A 2 04-AUG-1998;
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 Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
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 QY 181 TTCTCTGACTGGCCGCTCAGCTACAGTACCCAGGCTCAGCCAGCAGCAAGCTTACC 240
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DB      541 GGGGGCCCTGGTAACCTGTAGGGGCCCTTTTGTGTAGCAAG 579

RESULT 15
AC128940
LOCUS   AC128940
DEFINITION Rattus norvegicus clone CH230-43402, *** SEQUENCING IN PROGRESS
***, 4 unordered pieces.
AC128940.3 GI:25073546
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE   Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus
REFERENCE 1 (bases 1 to 220818)
AUTHORS Muzny,D,Marie., Metzker,M.Lee., Abranzon,S., Adams,C., Alder,J.,
          Allen,C., Allen,H., Alsdorfs,S., Amin,A., Arguiano,D.,
          Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
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Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 220818)
Worley,K.C.
Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 220818)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23269386.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KBEM
Center clone name: CH230-43402
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 202395 bases at least Q40
Consensus quality: 205627 bases at least Q30
Consensus quality: 207823 bases at least Q20
Estimated insert size: 212631; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.htm).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 174472: contig of 174472 bp in length
* 174573 174572: gap of unknown length
* 174573 218266: contig of 43694 bp in length
* 218267 218366: gap of unknown length
* 218367 219597: contig of 1231 bp in length
* 219598 219697: gap of unknown length
* 219698 220818: contig of 1121 bp in length.
Location/Qualifiers
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/db_xref="taxon:10116"
/clone="CH230-43402"
misc_feature 28851..30762
/notes="wgs_contig"
BASE COUNT 62390 a 42027 c 41606 g 62941 t 11854 others
ORIGIN
Query Match 80.5%; Score 468.4; DB 2; Length 220818;

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Best Local Similarity 89.5%; Pred. No. 3.7e-102;									
Matches 521; Conservative 0; Mismatches 46; Indels 15; Gaps 1;									
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QY	61	AGGCTGAGGACAGAGGGTTATCTGTGTGAGTGGCCCTGGGGAAGGCCACCCGCCGAC	120						
DB	142046	AAGCTGAGGTAGAGGGTTATGTGTGTGAGCTGSCCTGGGAAAGGCCACAGCTGAT	142105						
QY	121	CGGCTGACCAAGCCATCGGGCTCTGGAGAGAGTTTGAGACCCGTTTCGGCCGACCC	180						
DB	142106	CTGCTACACCAAGCCATCGATCTGTGAGACGAGTTTGAGACCCGCTTCGGGTACACC	142165						
QY	181	TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCAGGCTCAGCCACGCAACGCTTCACC	240						
DB	142166	TTCTCTGACCTAGCCACTCAGCAACATGTGACCCAGGCTCAGCCACGCAACGCTTCACC	142225						
QY	241	CAGGTTTCGACGAACTTTTCAAGGGGCCCTAACTGGGGCCGCTTTGTGGCAATCTTT	300						
DB	142226	CAGGTTTCGATGAACCTTTTCAAGGGGCCCCCAACTGGGACGCTCTGTGGCAATCTCT	142285						
QY	301	GTCTTTGGGGCTGCCCTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGSGA	360						
DB	142286	GTCTTTGGGGCTGCCCTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGSGA	142345						
QY	361	CAAGTCAAGGATTGGATGGTGGCCCTACCTGGAGACACGCTCTGGCTGACTGGATCCACGC	420						
DB	142346	CAAGTCAAGGACTGGATGGTGGCCCTACCTGGAGACATGCTGACTGACTGGATCCACGC	142405						
QY	421	AGTGGCGGCTGGCGGAGTTCAAGCTCTATACGGGACGGGGCCCTGGAGAGGCACGG	480						
DB	142406	AGTGGCGGCTGGCGGAGTTCAAGCTCAATACGAGACGGGGCCCTGGAGAGGTAC--	142463						
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QY	541	GGGGCCCTGGTAACCTGTAGGGCCCTTTTGTAGCAAGTGA	582						
DB	142511	GGAGCCCTGGTAACCTGTAGGGCCCTTTTGTAGCAAGTGA	142552						

Search completed: October 27, 2003, 13:01:26
Job time : 1737.01 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw mode.

Run on: October 27, 2003, 11:02:30 ; Search time 176.848 Seconds
(without alignments)
8883.744 Million cell updates/sec

Title: US-09-925-674a-8

Perfect score: 582
Sequence: 1 atggcgaccagcctcaac.....cctttttgtagcaagtgga 582

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5-05512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 3%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 18Jun03.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	577.8	99.3	581	20	Mouse bcl-w gene.
2	563.4	96.8	581	18	Mouse bcl-w DNA.
3	563.4	96.8	581	20	Mouse bcl-w gene d
4	558.2	95.9	579	19	Rat bcl-y gene. R
5	558.2	95.9	579	20	cDNA encoding the
6	524.4	90.1	582	24	Human bcl-w polynu
7	524.4	90.1	582	24	Human bcl-w DNA fr
8	524.4	90.1	582	24	Human bcl-w DNA SE

9	524.4	90.1	582	24	ABL91694	Human polynucleoti
10	521.2	89.6	3542	25	ABT16642	Human bcl-2 gene S
11	520.2	89.4	581	20	AAV25132	Human bcl-w gene.
12	519.6	89.3	583	18	AAV95577	Human bcl-w DNA.
13	519.6	89.3	583	20	AAV25134	Human bcl-w gene d
14	515	88.5	579	19	AAV28334	Human bcl-y gene.
15	515	88.5	579	20	AAV15946	cDNA encoding the
16	372.8	64.1	1098	19	AAV41925	Nucleotide sequenc
17	372.4	64.0	1864	19	AAV59630	Human secreted pro
18	372.4	64.0	1864	24	ABV73617	Human cDNA #1 for
19	372.4	64.0	1864	24	ABV73617	Human immune syste
20	372.4	64.0	1864	24	ABV73617	Human breast cell
21	372.4	64.0	1864	24	ABV73617	Human foetal liver
22	372.4	64.0	1864	24	ABV73617	Probe #0836 for g
23	372.4	64.0	1864	24	ABV73617	Human brain expres
24	372.4	64.0	1864	24	ABV73617	Human bone marrow
25	372.4	64.0	1864	24	ABV73617	Probe #0169 for g
26	372.4	64.0	1864	24	ABV73617	Probe #1424 used
27	372.4	64.0	1864	24	ABV73617	Probe #5931 used t
28	372.4	64.0	1864	24	ABV73617	Human liver single
29	372.4	64.0	1864	24	ABV73617	Human genome-deriv
30	372.4	64.0	1864	24	ABV73617	Rat wild-type bcl-
31	372.4	64.0	1864	24	ABV73617	Mutant bcl-XL codi
32	372.4	64.0	1864	24	ABV73617	cDNA clone HP3564
33	372.4	64.0	1864	24	ABV73617	Human thymus Bcl-X
34	372.4	64.0	1864	24	ABV73617	Bcl-Xl gene. Homo
35	372.4	64.0	1864	24	ABV73617	Bcl-x gene. Homo
36	372.4	64.0	1864	24	ABV73617	Human bcl-x cDNA.
37	372.4	64.0	1864	24	ABV73617	Human bcl-Xl nucle
38	372.4	64.0	1864	24	ABV73617	Human cDNA differe
39	372.4	64.0	1864	24	ABV73617	Human bcl-2 gene S
40	372.4	64.0	1864	24	ABV73617	Bcl-Xl-ETR apoptos
41	372.4	64.0	1864	24	ABV73617	Base sequence of t
42	372.4	64.0	1864	24	ABV73617	LFr-Bcl-Xl apoptos
43	372.4	64.0	1864	24	ABV73617	Human bcl-Xl (tran
44	372.4	64.0	1864	24	ABV73617	Human foetal liver
45	372.4	64.0	1864	24	ABV73617	

ALIGNMENTS

RESULT :
AAV25133 standard; DNA; 581 BP.

AC AAV25133;
05-JUL-1999 (first entry)

DE Mouse bcl-w gene.

KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
KW animal model; es.

CS Mus sp.

PN WO9913710-A1.

PD 25-MAR-1999.

PF 16-SEP-1998; 98WO-AU00764.

PR 16-SEP-1997; 97AU-0009228.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

PI Adams J, Cory S, Gibson L, Koentgen P, Print C;

DR WPI; 1999-243890/20.

DR P-PSDB; AAY05531.

PT An animal model exhibiting reduced levels of a Bcl-w protein and/or

PT protein associated with Bcl-w
PS Claim 3; Page 34; 52pp; English.

XX The present sequence is the mouse bcl-w gene encoding Bcl-w protein
CC (see AAY0531), a pro-survival member of the Bcl-2 family which is
CC widely expressed and which is essential for spermatogenesis. The
CC invention relates generally to a method of treatment and to an
CC animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male
CC animals. Methods are provided for the treatment of infertility, or
CC for reducing fertility, by modulating spermatogenesis. An animal
CC model carries a mutation in at least one allele of the human or
CC murine bcl-w gene or in a gene associated with bcl-w. Such animals
CC have disorganised seminiferous tubules and are substantially
CC infertile, but possess no other major abnormalities as determined
CC by histological examination. They can be used to screen for
CC therapeutic molecules including genetic sequences capable of
CC inducing, enhancing or otherwise facilitating spermatogenesis in
CC animals, or which can induce infertility.

SQ Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 other;

Query Match 99.3%; Score 577.8; DB 20; Length 581;
Best Local Similarity 99.1%; Pred. No. 2.9e-143;
Matches 579; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCACCCAGCCTCAACCCAGACACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
DB |||||
QY 61 AGCTGAGGAGAGAGGTTATGCTGTGAGTGGCTTGGGAGAGGCCAGCCGCCAC 120
DB |||||
QY 121 CCCTGCACCAAGCCATGCGGGTGTGAGACGAGTTGAGACCCGTTTCGCCGCACC 180
DB |||||
QY 181 TTCTGACCTGGCGCTCAGCTACAGTGAGCCAGGCTCAGCCAGCAAGCTTCACC 240
DB |||||
QY 241 CAGTTTCCGACCAACTTTTCCAGGGGGCCCTAACTGGGGCCGCTTGTGSCATCTTT 300
DB |||||
QY 301 GTCTTTGGGCTGCCCTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTTGTCGGGA 360
DB |||||
QY 361 CAGTGCAGGATTTGGATTTGGCTACCTGGAGACACAGTCTGGCTACGATGATCCACAGC 420
DB |||||
QY 421 AGTGGGGCTGGCGGAGTTACAGCTCTATACGGGACGGGGCCCTGGAGAGGACAGG 480
DB |||||
QY 481 CGTCTGGGAGGGGAACCTGGGATCAGTGAGACAGTCTCAGCGGGGCCCTGGCACTG 540
DB |||||
QY 541 GGGGCCCTGCTAACTGTAGGGGCCCTTTTGTGCAAGTG 581
DB |||||

RESULT 2
AAT96578
ID AAT96578 standard; DNA, 581 BP.

XX
AC AAT96578;

XX 22-APR-1998 (first entry)
XX Mouse bcl-w DNA.
XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
XX diagnosis; degenerative disease; ss.
XX Mus sp.
XX Key Location/Qualifiers
XX CDS 1..507
XX FT /*tag= a
XX FT /product= bcl-w
XX FT /note= "q"
XX WC9735971-Al.
XX 02-OCT-1997.
XX 27-MAR-1997; 97MO-AU00199.
XX 27-MAR-1996; 96AU-0008965.
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX Adams JM, Cory S, Gibson LM, Holmgren SP;
XX WPI: 1997-489635/45.
XX P-PSDB; AAW36048.
XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce
XX or inhibit cell survival, e.g. for treatment of cancer and
XX degenerative diseases
XX Claim 3; Page 50-51; 86pp; English.
XX This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene
XX family. This gene promotes cell survival, so its modulation is useful in
XX treatment of cancer or auto-immune diseases, degenerative diseases (e.g.
XX stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,
XX hypoxia, ischaemia, human immunodeficiency virus infection or in cell
XX transplants. Up-regulation of the gene can also be used to modify cell
XX lines cultured in vivo, e.g. to develop new lines, to facilitate
XX isolation of hybridomas and to increase survival of primary explants
XX during genetic modification. It can be used to produce recombinant Bcl-w
XX for therapy, diagnosis, antibody production or screening of potential
XX modulators.

SQ Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;

Query Match 95.8%; Score 563.4; DB 16; Length 581;
Best Local Similarity 98.1%; Pred. No. 1.9e-139;
Matches 570; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGGGACCCCGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
DB |||||
QY 61 AGCTGAGGAGAGGTTATGCTGTGAGTGGCTTGGGAGAGGCCAGCCGCCAC 120
DB |||||
QY 121 CGGCTGCACCAAGCCATGCGGGCTCTGAGACGAGTTTGTAGACCCGTTTCGCCGCACC 180
DB |||||
QY 181 TTCTGTGACCTGGCGCTCAGCTACAGTGAGCCAGGCTCAGCCAGCAAGCTTCACC 240
DB |||||
QY 241 CAGGTTTCCGACCAACTTTTCCAGGGGGCCCTAACTGGGGCCGCTTGTGSCATCTTT 300
DB |||||

Db 241 CAGGTTTCGACGAACTTTTCCAGGGGCCCTAACTGGGGCCGCTCTTGTGGCACTTCCTT 300
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 Db 301 GTCTTTGGGCTGCCCTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGGGA 360
 Qy 361 CAAGTCCAGGATTGGATGTGGCTTACCTGGAGACACAGTCTGGCTGACTGGATCCACAGC 420
 Db 361 CAAGTCCAGGATTGGATGTGGCTTACCTGGAGACACAGTCTGGCTGACTGGATCCACAGC 420
 Qy 421 AGTGGCGCTGGCGGAGTTCAGCTCTATACGGGACGGGCCCTGGAGAGGACACGG 480
 Db 421 AGTGGCGCTGGCGGAGTTCAGCTCTATACGGGACGGGCCCTGGAGAGGACACGG 480
 Qy 481 CGTCTCGGAGGAGGAACCTGGGATCAGTGAGGACAGTCTGACGGGGCCCTGGSCACTG 540
 Db 481 CGTCTCGGAGGAGGAACCTGGGATCAGTGAGGACAGTCTGACGGGGCCCTGGSCACTG 540
 Qy 541 GGGGCCCTGTAACTGTAGGGCCCTTTTGTGCTAGCAAGTG 581
 Db 541 GGGGCCCTGTAACTGTAGGGCCCTTTTGTGCTAGCAAGTG 581

RESULT 3

AAV25135 standard; DNA; 581 BP.

XX AC AAX25135;

XX 05-JUL-1999 (first entry)

XX Mouse bcl-w gene derivative.

XX Spermato genesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
 KW animal model; ss.

XX Mus sp.

PH Key Location/Qualifiers
 FT CDS 1..507
 FT /*tag= a

XX W09913710-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-AU00764.

XX 16-SEP-1997; 97AU-C009228.

XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX Adams J, Cory S, Gibson L, Koentgen F, Print C;

XX WPI; 1999-243890/20.

XX P-PSDB; AAY05533.

XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w

XX Disclosure; Page 38; 52pp; English.

XX The present sequence is described as a derivative of the mouse
 CC bcl-w gene (see AAX25133) and encodes Bcl-w protein (see AAY05533), a
 CC pro-survival member of the Bcl-2 family which is widely expressed,
 CC and which is essential for spermatogenesis. The invention relates
 CC generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for the
 CC inducing or reducing fertility of male animals. Methods are
 CC provided for the treatment of infertility, or for reducing
 CC fertility, by modulating spermatogenesis. An animal model carries
 CC a mutation is at least one allele of the human or murine bcl-w gene
 CC or in a gene associated with bcl-w. Such animals have disorganised

CC seminiferous tubules and are substantially infertile, but possess no
 CC other major abnormalities as determined by histological examination.
 CC They can be used to screen for therapeutic molecules including
 CC genetic sequences capable of inducing, enhancing or otherwise
 CC facilitating spermatogenesis in animals, or which can induce
 CC infertility.

XX SQ Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;

Query March 96.8%; Score 563.4; DB 20; Length 581;
 Best Local Similarity 98.1%; Pred. No. 1.9e-139;
 Matches 570; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ATGGGACCCCGAGCTCAACCCACACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
 Db 1 ATGGGACCCCGAGCTCAACCCACACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy 61 AGGCTGAGGACAGAGGGTTATCTGTGGAGCTGCCCTGGGGAAGGCCAGCCGCCAC 120
 Db 61 AGGCTGAGGACAGAGGGTTATCTGTGGAGCTGGGCTGGGGAAGGCCAGCCGCCAC 120

Qy 121 CGCTGCACCAAGCCATCGGGCTCTGGAGACGAGTTTGAGACCCGTTCCGCCGAC 180
 Db 121 CGCTGCACCAAGCCATCGGGCTCTGGAGACGAGTTTGAGACCCGTTCCGCCGAC 180

Qy 181 TTCTGTGACCTGGCGCTCAGTACAGTACCCAGGCTAGCCAGCAAGCTTCACC 240
 Db 181 TTCTGTGACCTGGCGCTCAGTACAGTACCCAGGCTAGCCAGCAAGCTTCACC 240

Qy 241 CAGGTTTCGACGAACTTTTCCAGGGGCCCTAACTGGGGCCGCTCTTGTGGCATTCTTT 300
 Db 241 CAGGTTTCGACGAACTTTTCCAGGGGCCCTAACTGGGGCCGCTCTTGTGGCATTCTTT 300

Qy 301 GTCTTTGGGCTGCCCTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGGGA 360
 Db 301 GTCTTTGGGCTGCCCTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGGGA 360

Qy 361 CAAGTCCAGGATTGGATGTGGCTTACCTGGAGACACAGTCTGGCTGACTGGATCCACAGC 420
 Db 361 CAAGTCCAGGATTGGATGTGGCTTACCTGGAGACACAGTCTGGCTGACTGGATCCACAGC 420

Qy 421 AGTGGCGCTGGCGGAGTTCAGCTCTATACGGGACGGGCCCTGGAGAGGACACGG 480
 Db 421 AGTGGCGCTGGCGGAGTTCAGCTCTATACGGGACGGGCCCTGGAGAGGACACGG 480

Qy 481 CGTCTCGGAGGAGGAACCTGGGATCAGTGAGGACAGTCTGACGGGGCCCTGGSCACTG 540
 Db 481 CGTCTCGGAGGAGGAACCTGGGATCAGTGAGGACAGTCTGACGGGGCCCTGGSCACTG 540

Qy 541 GGGGCCCTGTAACTGTAGGGCCCTTTTGTGCTAGCAAGTG 581
 Db 541 GGGGCCCTGTAACTGTAGGGCCCTTTTGTGCTAGCAAGTG 581

RESULT 4

AAV28333 standard; cDNA; 579 BP.

XX AC AAV28333;

XX 02-OCT-1998 (first entry)

XX Rat bcl-y gene.

XX ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.

XX Rattus sp.

PH Key Location/Qualifiers
 FT CDS 1..579
 FT /*tag= a
 FT /product= bcl-y
 FT /note= "No stop codon given"

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XX US5789201-A.
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XX 11-FEB-1997; 97US-0798897.
XX
XX 23-FEB-1996; 96US-0012201.
XX 11-FEB-1997; 97US-0798897.
XX
XX (COCE-) COCENSYS INC.
XX
XX Guastella J;
XX
XX WPI; 1998-446079/38.
XX
XX P-PSDB; AAW6:391.
XX
XX Nucleic acids encoding B-cell lymphoma-y protein - useful for
XX producing recombinant protein for use in treating uncontrolled cell
XX growth e.g. cancers
XX
XX Claim 2; Column 13/14; 27pp; English.
XX
XX The mammalian bcl-y genes encode a protein that is a member of the bcl-2
XX family, components in the cell death pathway. The bcl-2 family
XX have both apoptotic activity and the apoptosis blocking activity. bcl-y
XX falls in the apoptosis activity category. The recombinant protein may
XX be used to prevent uncontrolled cell growth, either by its direct
XX administration to recombinant genetic constructs to increase its
XX expression in vivo. Also, antisense constructs can be used in disorders
XX where prevention of cell death is desired.
XX
XX Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;
XX
XX Query Match 95.9%; Score 558.2; DB 19; Length 579;
XX Best Local Similarity 97.8%; Pred. No. 4.4e-133;
XX Matches 566; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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Qy 1 ATGGGACCCAGGCTCAACCCAGACACACGGGCTTAGTGGCTGACTTTGTAGGCTAT 60
Db 1 ATGGGACCCAGGCTCAACCCAGACACACGGGCTTAGTGGCTGACTTTGTAGGCTAT 60
Qy 61 AGGCTGAGGACAGAGGGTTATGCTGTGAGCTGGCTGGGAGGCCAGCCGCGAC 120
Db 61 AAGCTGAGACAGAGAGGGTTATGCTGTGAGCTGGCTGGGAGGCCAGCCGCGAC 120
Qy 121 CCGTGTGACCAAGCCATCGGGGCTCTGGAGACGAGTTTGAGACCCGTTTCCGCGCCACC 180
Db 121 CCGTGTGACCAAGCCATCGGGGAGCTGGAGACGAGTTTGAGACCCGCTTCCGGGCGACC 180
Qy 181 TTCTGTGACCTGGCGGCTCAGCTACCTGACCCAGGCTCAGCCGAGCAACGGTTTCAACC 240
Db 181 TTC-CTGACCTGGCGGCTCAGCTACCTGACCCAGGCTCAGCCGAGCAACGGTTTCAACC 240
Qy 241 CAGGTTCCGAGCAGACTTTCCAGGGGGCCCTTACCTGGGGCCCTCTGTGCGATCTTT 300
Db 241 CAGGTTTCCGAGCAGACTTTTCCAGGGGGCCCTTACCTGGGGCCCTCTGTGCGATCTTT 300
Qy 301 GTCTTTGGGGTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCCTTTGGTGGGA 360
Db 301 GTCTTTGGGGTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCATTTGGTGGGA 360
Qy 361 CAAGTGCAAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 CAAGTGCAAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Qy 421 AGTGCGCGCTGGCGGAGCTTCAAGCTCTATACGGGGACGGGGCCCTTGGAGAGGACGG 480
Db 421 AGTGCGCGCTGGCGGAGCTTCAAGCTCTATACGGGGACGGGGCCCTTGGAGAGGACGG 480
Qy 481 CTTCTGCGGGAGGGGAACTGGGCACTCAGTGAGGACAGTGTCTGACGGGGGCGCTGGCACTG 540
Db 481 CTTCTGCGGGAGGGGAACTGGGCACTCAGTGAGGACAGTGTCTGACGGGGGCGCTGGCACTG 540
```

```
Cy 541 GGGGCCCTGTAACCTGATAGGGCCCTTTTGTCTAGCAAG 579
Db 541 GGGGCCCTGTAACCTGATAGGGCCCTTTTGTCTAGCAAG 579

RESULT 5
AA15945
ID AAX15945 standard; cDNA; 579 BP.
XX
XX AAX15945;
XX
XX 20-MAY-1999 (first entry)
XX
XX cDNA encoding the rat bcl-y protein.
XX
XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
XX head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
XX multiple sclerosis; myocardial infarction; vitally induced cell death;
XX aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
XX premature cell death; cell death stimulator; prolonged cell life span;
XX Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
XX parasite; ss.
XX
XX Rattus sp.
XX
XX US5883229-A.
XX
XX 16-MAR-1999.
XX
XX 25-NOV-1997; 97US-0978523.
XX
XX 23-FEB-1996; 96US-0012201.
XX 11-FEB-1997; 97US-0798897.
XX 25-NOV-1997; 97US-0978523.
XX
XX (COCE-) COCENSYS INC.
XX
XX Guastella J;
XX
XX WPI; 1999-214150/18.
XX P-PSDB; AAW57391.
XX
XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful
XX for modulating programmed cell death
XX
XX D:sclosure; Columns 13-16; 26pp; English.
XX
XX The present sequence encodes rat bcl-y protein (Rbcl-y). The
XX specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
XX Hbcl-y are homologues of the bcl-2 protein thought to be involved in
XX programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
XX proteins may be used to treat conditions associated with a disruption of
XX the cell death pathway. If they act as cell death inhibitors, they may be
XX used in therapies to treat subjects suffering from: strokes, head trauma,
XX Alzheimer's Disease, neural and muscular degenerative diseases
XX (especially multiple sclerosis), myocardial infarction, vitally induced
XX cell death, aging, spinal cord injuries and amyotrophic lateral
XX sclerosis- conditions where cells under go premature cell death as a
XX result of triggers which may or may not be apparent. They may also be
XX used in this way to develop cell lines which remain viable in culture for
XX an extended period. In contrast, if they act as cell death stimulators,
XX Rbcl-y and Hbcl-y may be used to treat conditions associated with
XX prolonged cell life span such as cancer (especially Kaposi's sarcoma and
XX lung cancer) and auto/hyperimmune diseases. They may also be used to
XX cause cell death in, and hence control, parasites.
XX
XX Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;
XX
XX Query Match 95.9%; Score 558.2; DB 20; Length 579;
XX Best Local Similarity 97.8%; Pred. No. 4.4e-138;
XX Matches 566; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
```


ABX09972;
 23-JAN-2003 (first entry)
 Human bcl-w DNA fragment SEQ ID 37.
 oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;
 prion; inhibition; human; ds.
 Homo sapiens.
 DE10100587-Cl.
 21-NOV-2002.
 09-JAN-2001; 2001DE-1000587.
 09-JAN-2001; 2001DE-1000587.
 (RIBO-) RIBOPHARMA AG.
 Kreutzer R, Limmer S, Rost S, Hadwiger P;
 WPI: 2002-742209/81.
 Inhibiting expression of target genes, e.g. oncogenes, in cells, by
 introduction of complementary double-stranded oligoribonucleotide,
 after treating the cell with interferon -
 Disclosure; Page 35-36; 98pp; German.
 This invention describes a novel method for inhibiting expression of a
 target gene by introducing into the cell that contains the target gene
 at least one oligoribonucleotide (dsRNA) that has a double-stranded
 (ds) structure of not more than 49 consecutive nucleotides (nt), where
 at least a segment of one strand of the ds structure is complementary
 with the target gene and the cells are treated with interferon before
 introduction of dsRNA. The method is used to inhibit expression of
 target genes, particularly oncogenes, cytokine genes, Id (not defined;
 protein genes; developmental or prion genes, or genes expressed in
 pathogenic organisms (particularly plasmodia) or in viruses or viroids
 (pathogenic in humans, animals or plants). Treating the cells with
 interferon greatly increases the extent to which dsRNA can inhibit
 expression of the target genes, and the effect is even greater when dsRNA
 are modified to increase their stability. ABX09936-ABX10075 represent
 gene fragments used to illustrate the method of the invention.
 Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 other;
 Query Match
 Best Local Similarity 90.1%; Score 524.4; DB 24; Length 582;
 Matches 546; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 QY 1 ATGCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTAGGCTAT 60
 Db 1 ATGCGACCCAGCCTCGGCCCCAGACACACGCGCTCTGCTGCGAGACTTTGTAGGTAT 60
 QY 61 AGGCTGAGCAGAGGGTTATGCTCTGGAGCTGGCCCTGGGAGGCCCGCGGAC 120
 Db 61 AAGCTGAGCAGAGGGTTATGCTCTGGAGCTGGCCCTGGGAGGCCCGCGGAGCTGAC 120
 QY 121 CCGCTGCACCAAGCATCGGGCTGGTGGAGACGAGTTTCAGACCCGCTTCCCGCCGAC 180
 Db 121 CCGCTGCACCAAGCATCGGGCTGGTGGAGACGAGTTTCAGACCCGCTTCCCGCCGAC 180
 QY 181 TTCTGTACCTGGCGCTACGTACAGTACCCAGGCTCAGCCAGCAACGCTTCACC 240
 Db 181 TTCTGTATCTGGCGGCTACGTATGATGACCCAGGCTCAGCCAGCAACGCTTCACC 240
 QY 241 CAGGTTCCGACGAACTTTTCCAGAGGGGGCCCTTAACCTGGGGCGCTTTGGGCACTCTT 300
 Db 241 CAGGTTCCGACGAACTTTTCCAGAGGGGGGCCCAACTGGGGCGCCCTTTGAGCCCTCTT 300

QY 301 GTCTTTGGGGCTGCCCTGTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCCTTTGGTGGGA 360
 Db 301 GTCTTTGGGGCTGCACCTGTGTGTGCTGAGAGTGTCAACAAAGAGATGGAACCACTGGTGGGA 360
 QY 361 CAAGTGCAGGATTTGGATGGTGGCTTACCTGAGAGACAGCTGTGGCTGACTGATCCACAGC 420
 Db 361 CAAGTGCAGGATTTGGATGGTGGCTTACCTGAGAGACAGCTGTGGCTGACTGATCCACAGC 420
 QY 421 AGTGGCGGCTGGGCGGAGTTTACAGAGCTCTATACGGGACCGGGCCCTGGAGAGGACGCG 480
 Db 421 AGTGGGCTGGGCGGAGTTTACAGAGCTCTATACGGGACCGGGCCCTGGAGAGGCGCGG 480
 QY 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAGGACACTGTGACGGGGCGGCTG33CACTG 540
 Db 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAGGACACTGTGACGGGGCGGCTGGCACTG 540
 QY 541 GGGGCCCTGGTAAGTGTAGGGGCGCTTTTGTCTAGCAAGTGA 582
 Db 541 GGGGCCCTGGTAAGTGTAGGGGCGCTTTTGTCTAGCAAGTGA 582
 RESULT 8
 ABV78153
 ID ABV78153 standard; DNA; 582 BP.
 XX AC ABV78153;
 XX 15-NOV-2002 (first entry)
 XX Human bcl-w DNA SEQ ID NO 37.
 XX RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;
 KW virucide; protozoacide; gene; ds.
 OS Homo sapiens.
 PN WO200255693-A2.
 XX PD 18-JUL-2002.
 XX C9-JAN-2002; 2002WO-EP00152.
 XX C9-JAN-2001; 2001DE-1000586.
 PR 26-OCT-2001; 2001DE-1055280.
 PR 29-NOV-2001; 2001DE-1058411.
 PR 07-DEC-2001; 2001DE-1060151.
 XX (RIBO-) R-BOPHARMA AG.
 XX Kreutzer R, Limmer S, Rost S, Hadwiger P;
 XX WPI: 2002-590671/63.
 XX Inhibiting expression of target gene, useful e.g. for inhibiting
 PT oncogenes, by administering double-stranded RNA complementary to the
 PT target and having an overhang -
 PS Claim 10; Page 134; 203pp; German.
 XX The invention relates to inhibiting expression of a target gene (i) in a
 CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded
 CC structure of at most 49 consecutive bases. At least part of one strand
 CC (asi) of dsRNA is complementary to (i) and at least one end of dsRNA
 CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
 CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
 CC in humans, also genes in plasmodium or in viruses or viroids that are
 CC pathogenic for humans, animals or plants. Introducing an overhang into
 CC dsRNA greatly increases effectiveness for inhibiting gene expression,
 CC both in vivo and in vitro and also increases stability and thus the
 CC effective concentration inside the cell. The present sequence is that of
 CC a gene related to the invention.
 XX Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 other;

RESULT 10
ABT16642

ID ABL16642 standard; DNA; 3542 BP.
 AC ABL16642;
 XX
 XX 03-APR-2003 (first entry);
 XX
 DE Human bcl-2 gene SEQ ID No 4.
 XX
 XX Anti-tumour; DNazyme; bcl-2 gene; tumour; malignant; chemotherapy;
 XX radiation therapy; catalytic domain; enzyme; human; ds.
 XX
 XX Homo sapiens.
 XX WO200299090-A1.
 XX
 XX 12-DEC-2002.
 XX
 XX 07-JUN-2002; 2002WO-AU00739.
 XX
 XX 07-JUN-2001; 2001AU-0005527.
 XX (JOHN J JOHNSON & JOHNSON RES PTY LTD.
 XX Sun L, Wang L, Turner RJ, Saravolac EG, Dass CR;
 XX WPI; 2003-140617/13.
 DR
 XX Novel DNazyme useful for treating tumors, and for enhancing the
 XX sensitivity of malignant or virus infected cells to therapy, comprises
 XX a catalytic domain and binding domain contiguous to the catalytic
 XX domain -
 XX
 XX Disclosure; Page 44-45; 67pp; English.
 XX
 XX The invention relates to a DNazyme which specifically cleaves mRNA
 XX transcribed from a member of the bcl-2 gene family. The DNazymes comprise
 XX a catalytic domain, binding domains contiguous with the 5' and 3' end of
 XX the catalytic domain, and therefore hybridise with, the two regions
 XX immediately flanking the purine residue of the cleavage site within the
 XX bcl-2 gene family mRNA, at which DNazyme-catalysed cleavage is desired. A
 XX pharmaceutical composition comprising a DNazyme of the invention is
 XX useful for treating tumours in a subject, and for enhancing the
 XX sensitivity of malignant or virus infected cells to therapy.
 XX The DNazymes are useful in diagnostics, therapeutics,
 XX prophylaxis, research agents and in kits. The DNazymes are also
 XX useful for increasing the susceptibility of tumour cells to anti-tumour
 XX therapies such as chemotherapy and radiation therapy. This polynucleotide
 XX sequence represents a human bcl-2 gene of the invention.
 XX
 XX Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 other;
 XX
 XX Query March 89.6%; Score 521.2; DB 25; Length 3542;
 XX Best Local Similarity 93.5%; Pred. No. 4.7e-128;
 XX Matches 544; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
 XX
 XX 1 ATGGCGACCCAGCCCTCAACCCACAGACACACGCGTCTAGTGGCTGACTTTGTAGGCTAT 60
 XX
 XX 177 ATGGCGACCCAGCCCTCGGCCCCACAGACACACGCGTCTGGTGGCAGACTTTGTAGGTTAT 236
 XX
 XX 61 AGCTGAGCGAGNAGGTTATGCTCTGTGAGTGGCTGCGGAGGCGCCAGCCGCGAC 120
 XX
 XX 237 AAGCTGAGCGAGNAGGTTATGCTCTGTGAGTGGCTGCGGAGGCGCCAGCAGCTGAC 296
 XX
 XX 121 CCCTGTGACCAACCCAGCCCTCGCGGCTGCTGGAGACGAGTTTGACACCCGTTCCGCGGCACC 180
 XX
 XX 297 CCCTGTGACCAACCCAGCCCTCGCGGCTGCTGGAGACGAGTTTGACACCCGTTCCGCGGCACC 356
 XX
 XX 181 TTCTGTGACTGCGCGCTCAGCTACAGTGAGCCAGGCTCAGCCAGCAGCGTTTCAAC 240
 XX
 XX 357 TTCTGTGACTGCGCGCTCAGCTACAGTGAGCCAGGCTCAGCCAGCAGCGTTTCAAC 416
 XX
 XX 241 CAGGTTTCCGACCAACTTTTCCAAAGGGGCGCTTAAGTGGGCGCGTCTGTGGCATCTCTTT 300

Db 417 CAGGTCTCCGATGAACCTTTTTCAGGGGGCCCCCAACTGGGGGGCGCTTGTAGCTTCTT 476
 Qy 301 GTCTTTGGGCTGCCCTGTGTGTGTGAGAGTGTCAACAAAGATGAGAGCTTTTGTGGGA 360
 Db 477 GTCTTTGGGCTGCCCTGTGTGTGTGAGAGTGTCAACAAAGATGAGAGCTTTTGTGGGA 536
 Qy 361 CAAGTGACAGGATTGGATGGTGGCTTACCTGGAGACACCTCTGGCTGACTGATCCACAGC 420
 Db 537 CAAGTGACAGGATTGGATGGTGGCTTACCTGGAGACACCTCTGGCTGACTGATCCACAGC 596
 Qy 421 AGTGGCGCTGGGCGGAGTTTCAAGCTCTATACGGGACCGGGCCCTGGAGAGGACCGG 480
 Db 597 AGTGGCGCTGGGCGGAGTTTCAAGCTCTATACGGGACCGGGCCCTGGAGAGGAGCGG 656
 Qy 481 CGTCTGCGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTGACGGGGCGCTGGCACTG 540
 Db 657 CGTCTGCGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTGACGGGGCGCTGGCACTG 716
 Qy 541 GGGGCCCTGGTAACTGTAGGGGCGCTTTTGTGCTAGCAAGTGA 582
 Db 717 GGGGCCCTGGTAACTGTAGGGGCGCTTTTGTGCTAGCAAGTGA 758
 XX
 XX RESULT 11
 XX AAX25132
 XX ID AAX25132 standard; DNA; 581 BP.
 XX AC AAX25132;
 XX XX
 XX 05-JUL-1999 (first entry)
 XX XX
 XX Human bcl-w gene.
 XX XX
 XX Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
 XX animal model; ss.
 XX OS Homo sapiens.
 XX PN WO99:3710-A1.
 XX XX
 XX 25-MAR-1999.
 XX XX
 XX 16-SEP-1999; 98WO-AU00764.
 XX XX
 XX 16-SEP-1997; 97AU-0009228.
 XX XX
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX PA
 XX Adams J, Cory S, Gibson L, Koentgen F, Print C;
 XX PI
 XX WPI; 1999-243890/20.
 XX DR
 XX P-PSDB; AAY05530.
 XX XX
 XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
 XX protein associated with Bcl-w
 XX
 XX Claim 3; Page 32; 52pp; English.
 XX
 XX The present sequence is the human bcl-w gene encoding Bcl-w protein
 XX (see AAY05530), a pro-survival member of the Bcl-2 family which is
 XX widely expressed and which is essential for spermatogenesis. The
 XX invention relates generally to a method of treatment and to an
 XX animal model for the identification of molecules and genetic
 XX sequences useful for inducing or reducing fertility of male
 XX animals. Methods are provided for the treatment of infertility, or
 XX for reducing fertility, by modulating spermatogenesis. An animal
 XX model carries a mutation is at least one allele of the human or
 XX murine bcl-w gene or in a gene associated with bcl-w. Such animals
 XX have disorganised seminiferous tubules and are substantially
 XX infertile, but possess no other major abnormalities as determined
 XX by histological examination. They can be used to screen for
 XX therapeutic molecules including genetic sequences capable of
 XX inducing, enhancing or otherwise facilitating spermatogenesis in.

Db 541 GGGGCCCTGGTAAGTGTAGGGGCGCTTTTGTCTAGCAAGTGA 582

RESULT 13

AAV28334

ID AAV28334 standard; DNA; 583 BP.

XX AC AAV28334;

XX DT 05-JUL-1999 (first entry)

XX DE Human bcl-w gene derivative.

XX KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;

XX KW animal model; ss.

XX OS Homo sapiens.

XX PN WO9913710-A1.

XX PD 25-MAR-1999.

XX PF 16-SEP-1998; 98WO-AU00764.

XX PR 16-SEP-1997; 97AU-0009228.

XX PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX PI Adams J, Cory S, Gibson L, Koentgen P, Print C;

XX DR WPI; 1999-243890/20.

XX DR P-PSDB; AAY05532.

XX PT An animal model exhibiting reduced levels of a Bcl-w protein and/or

XX PS protein associated with Bcl-w

XX PS Disclosure; Page 36; 52pp; English.

XX CC The present sequence is described as a derivative of the human

CC bcl-w gene (see AAY05532) and encodes Bcl-w protein (see AAY05532); a

CC pro-survival member of the Bcl-2 family which is widely expressed

CC and which is essential for spermatogenesis. The invention relates

CC generally to a method of treatment and to an animal model for the

CC identification of molecules and genetic sequences useful for

CC inducing or reducing fertility of male animals. Methods are

CC provided for the treatment of infertility, or for reducing

CC fertility, by modulating spermatogenesis. An animal model carries

CC a mutation is at least one allele of the human or murine bcl-w gene

CC or in a gene associated with bcl-w. Such animals have disorganised

CC seminiferous tubules and are substantially infertile, but possess no

CC other major abnormalities as determined by histological examination.

CC They can be used to screen for therapeutic molecules including

CC genetic sequences capable of inducing, enhancing or otherwise

CC facilitating spermatogenesis in animals, or which can induce

XX CC infertility.

XX SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;

Query Match 69.3%; Score 519.6; DB 20; Length 583;

Best Local Similarity 93.3%; Pred. No. 7.4e-128;

Matches 543; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGAGCTCAACCCGAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

DB 1 ATGGCGACCCAGAGCTCTGGCCCCGAGACACACGGGCTCTGGTGGCAGACTTTGTAGGCTAT 60

QY 61 AGGCTGAGCGCAGAGGGGTATGTCTGTGGAGCTGGCCCTGGGGAAGCCAGCGCGGCAC 120

DB 61 AAGCTGAGCGCAGAGGGGTATGTCTGTGGAGCTGGCCCTGGGGAAGCCAGCGAGCTGAC 120

QY 121 CCGTGTACCAAGCATCGGGCTGTCTGGAGACGAGTTTGAGACCCGTTTCCGCGCACC 180

DB 121 CCGTGTACCAAGCATCGGGCAGCTGGAGATGAGTTTCGAGACCCGCTTCCGCGCACC 180

QY 181 TTCTGTGACCTGGCCGCTCAGCTACAGTACGCCAGGCTCAGCCAGCAACGCTTCACC 240
DB 181 TTCTGTGATCTGGCGGCTCAGCTGATGACCCAGGCTCAGCCAGCAACGCTTCACC 240
QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTAACTGGGGCCGCTTTTGTGGCACTTTT 300
DB 241 CAGGTCTCCGACGAACTTTTCCAAAGGGGGCCCAACTGGGGCCGCTTTGTAGCTTTT 300
QY 301 GTCCTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGGGA 360
DB 301 CTCCTTGGGGCTGCACGTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
QY 361 CAAGTGACAGGATTTGGATGGTGGCCCTACCTGGAGACACGCTCTGGCTGACTGGATCCACAGC 420
DB 361 CAAGTGACAGGATTTGGATGGTGGCCCTACCTGGAGACGCGCTGGTGGATCCACAGC 420
QY 421 AGTGGCGCTGGGCGGAGTTTCAAGCTCTATACGGGACCGGGCCCTTGGAGGAGGACGG 480
DB 421 AGTGGGGCTGGGCGGAGTTTCAAGCTCTATACGGGACCGGGCCCTTGGAGGAGGCGCG 480
QY 481 CGTCTGGCGGAGGGGAAGTGGGCACTCAGTGAGGACAGTGTGCTGACGGGGCGCTGGCACTG 540
DB 481 CGTCTGGCGGAGGGGAAGTGGGCACTCAGTGAGGACAGTGTGCTGACGGGGCGCTGGCACTG 540
QY 541 GGGGCCCTGGTAAGTGTAGGGGCGCTTTTGTCTAGCAAGTGA 582
DB 541 GGGGCCCTGGTAAGTGTAGGGGCGCTTTTGTCTAGCAAGTGA 582

RESULT 14

AAV28334

ID AAV28334 standard; cDNA; 579 BP.

XX AC AAV28334;

XX DT 02-OCT-1998 (first entry)

XX DE Human bcl-y gene.

XX KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.

XX OS Homo sapiens.

XX FH Key

XX CDS

XX Location/Qualifiers

XX 1..579

XX /*tag= a

XX /product= bcl-y

XX /note= "No stop codon given"

XX US5789201-A.

XX 04-AUG-1998.

XX 11-FEB-1997; 97US-0798897.

XX 23-FEB-1996; 96US-0012201.

XX 11-FEB-1997; 97US-0798897.

XX (COCE-) COCENSYS INC.

XX Guastella J;

XX WPI; 1998-446079/38.

XX P-PSDB; AAW61392.

XX Nucleic acids encoding B-cell lymphoma-y protein - useful for

XX producing recombinant protein for use in treating uncontrolled cell

XX growth e.g. cancers

XX Claim 3; Column 15/16; 27pp; English.

XX The mammalian bcl-y genes encode a protein that is a member of the bcl-2

CC

CC family, components in the cell death pathway. The bcl-2 family
CC have both apoptotic activity and the apoptosis blocking activity. bcl-y
CC falls in the apoptosis activity category. The recombinant protein may
CC be used to prevent uncontrolled cell growth, either by its direct
CC administration to recombinant genetic constructs to increase its
CC expression in vivo. Also, antisense constructs can be used in disorders
CC where prevention of cell death is desired.

XX Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

Query Match 88.5%; Score 515; DB 19; Length 579;
Best Local Similarity 93.1%; Pred. No. 1.2e-126;
Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCAACCCGACACACACGGGCTCTAGTGGCTGACTTTGAGGCTAT 60
DB |||||
QY 61 AGGCTGAGGAGAGGGTTATGTCGTGGAGCTGGCCCTGGGAAGCCCGAGCGCGGAC 120
DB |||||
QY 61 AAGCTGAGGAGAGGGTTATGTCGTGGAGCTGGCCCGGGAGGCCCGAGAGCTGAC 120
DB |||||
QY 121 CCGCTGACCAAGCCATGCGGGCTGCTGGAGACAGTTTGAGACCCGTTTCCCGCCACC 180
DB |||||
QY 121 CCACTGACCAAGCCATGCGGGCAGCTGGAGATGAGTTGAGACCCGCTTCCGGGCAAC 180
DB |||||
QY 181 TTCTCTGACCTGGCGGCTCAGCTACACGTGACCCCGAGGCTCAGCCGAGCAAGCTTCACC 240
DB |||||
QY 181 TTCTCTGATCTGGCGGCTCAGCTGATGTCGAGCTGGCCCGGGAGGCCCGAGAGCTTCACC 240
DB |||||
QY 241 CAGGTTTCCGACGAACCTTTTCAAGGGGGGCCCTAACCTGGGCGGCTCTTGAGGATCTTT 300
DB |||||
QY 241 CAGGTTTCCGATGACCTTTTCAAGGGGGGCCCTAACCTGGGCGGCTCTTGAGGATCTTT 300
DB |||||
QY 301 GTCTTTGGGCTGCCCTGTGTGTGAGAGTGTCAACAAGAAATGAGCCCTTTGGTGGGA 360
DB |||||
QY 301 GTCTTTGGGCTGCACGTGTGTGTGAGAGTGTCAACAAGAGATGGAACACCTGGTGGGA 360
DB |||||
QY 361 CAAGTCAGAGATTGGATGGTGGCTTACTGTGAGACAGCTCTGCTGACTGGATCCACAGC 420
DB |||||
QY 361 CAAGTCAGAGATTGATGGTGGCTTACTGTGAGACAGCTCTGCTGACTGGATCCACAGC 420
DB |||||
QY 421 AGTGGCGGCTGGGGGAGTGTACAGCTCTATACGGGACCGGGCCCTGGAGAGGAGCGG 480
DB |||||
QY 421 AGTGGCGGCTGGGGGAGTGTACAGCTCTATACGGGACCGGGCCCTGGAGAGGAGCGG 480
DB |||||
QY 481 CGTCTGCGGAGGGAACTGGGCACTAGTGAGGACAGTGTGAGCGGGCGCTGGCACTG 540
DB |||||
QY 481 CGTCTGCGGAGGGAACTGGGCACTAGTGAGGACAGTGTGAGCGGGCGCTGGCACTG 540
DB |||||
QY 541 GGGGCGCTGCTACTGTAGGGGCTTTTCTAGCAAG 579
DB |||||
QY 541 GGGGCGCTGCTACTGTAGGGGCTTTTCTAGCAAG 579
DB |||||

RESULT 15

AAAX15946

ID: AAX15946 standard; cDNA; 579 BP.

XX AAX15946;

XX AC

XX DT

XX 20-MAY-1999 (first entry)

DE cDNA encoding the human bcl-y protein.

XX Rat bcl-y protein; Bcl-y; human bcl-y protein; Bcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW parasite; ss.

XX Homo sapiens.
XX US5853229-A.
XX 16-MAR-1999.
XX 25-NOV-1997; 97US-0978523.
XX 23-FEB-1996; 96US-0012201.
XX 11-FEB-1997; 97US-0798897.
XX 25-NOV-1997; 97US-0978523.
XX (COSE-) COSENSYS INC.
XX Quastelia J;
XX WP: 1999-214150/18.
XX P-PSDB; AAW97392.

Novel bcl-y homologues of the rat and human bcl-2 protein - useful
for modulating programmed cell death

Disclosure; Columns 15-16; 26pp; English.

The present sequence encodes human bcl-y protein (Bcl-y). The
specification also describes rat bcl-y protein (Bcl-y). Bcl-y and
Bcl-y are homologues of the bcl-2 protein thought to be involved in
programmed cell death (apoptosis and necrosis). Bcl-y and Bcl-y
proteins may be used to treat conditions associated with a disruption of
the cell death pathway. If they act as cell death inhibitors, they may be
used in therapies to treat subjects suffering from: strokes, head trauma,
Alzheimer's Disease, neural and muscular degenerative diseases
(especially multiple sclerosis), myocardial infarction, vitally induced
cell death, aging, spinal cord injuries and amyotrophic lateral
sclerosis- conditions where cells under go premature cell death as a
result of triggers which may or may not be apparent. They may also be
used in this way to develop cell lines which remain viable in culture for
an extended period. In contrast, if they act as cell death stimulators,
Bcl-y and Bcl-y may be used to treat conditions associated with
prolonged cell life span such as cancer (especially Kaposi's sarcoma and
lung cancer) and auto/hyperimmune diseases. They may also be used to
cause cell death in, and hence control, parasites.

XX Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

Query Match 88.5%; Score 515; DB 20; Length 579;
Best Local Similarity 93.1%; Pred. No. 1.2e-126;
Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCAACCCGACACACGGGCTCTAGTGGCTGACTTTGAGGCTAT 60
DB |||||
QY 1 ATGGCGACCCAGCCTCGGGCCCCGACACACGGGCTCTGGTGAAGACTTTGTAGGTTAT 60
DB |||||
QY 61 AGGCTGAGGAGAGGGTTATGTCGTGGAGCTGGCCCTGGGAGGCGCCAGCCCGGAC 120
DB |||||
QY 61 AAGCTGAGGAGAGGGTTATGTCGTGGAGCTGGCCCGGGAGGGGCCAGCAGCTGAC 120
DB |||||
QY 121 CCGCTGACCAAGCCATGCGGGCTGCTGGAGACAGTTTGAGACCCGTTTCCCGCGCAC 180
DB |||||
QY 121 CCACTGACCAAGCCATGCGGGCAGCTGGAGATGAGTTTCGAGACCCGCTTCCGGCGCAC 180
DB |||||
QY 181 TTCTCTGACCTGGCGGCTCAGCTACACGTGACCCCGAGGCTCAGCCGAGCAAGCTTCACC 240
DB |||||
QY 181 TTCTCTGATCTGGCGGCTCAGCTGATGACCCCGAGGCTCAGCCCAACAGCTTCACC 240
DB |||||
QY 241 CAGGTTTCCGAGACTTTTCCAGGGGGCCCTTACTGGGCGGCTTGTGGCATCTTT 300
DB |||||
QY 241 CAGGTTTCCGATGAACTTTTCAAGGGGGGCCCTTCAAGGGCGGCTTGTAGCCCTCTTT 300
DB |||||
QY 301 GTCTTTGGGCGCTGCCCTGTGTGTGAGAGTGTCAACAAGAAATGAGGCTTTGGTGGGA 360
DB |||||
QY 301 GTCTTTGGGCGTCACTGTGTGTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360
DB |||||

Qy	361	CAAGTCAGGATTGGATGGTGGCCCTACCTGGAGACACAGTCTGGCTGACTGGATCCACAGC	420
Db	361	CAAGTCAGGAGTGGATGGTGGCCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC	420
Qy	421	AGTGGCGGCTGGGCGGAGTTTCACAGCTCTATACGGGACGCGGCCCTGGAGGAGGCACGG	480
Db	421	AGTGGGCGCTGGGCGGAGTTTCACAGCTCTATACGGGACGCGGCCCTGGAGGAGGCACGG	480
Qy	481	CGTCTGGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCGCGTGGCACTG	540
Db	481	CGTCTGGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCGCGTGGCACTG	540
Qy	541	GGGCGCTGTACTGTAGGGCCCTTTTGTAGCAAG	579
Db	541	GGGCGCTGTACTGTAGGGCCCTTTTGTAGCAAG	579

Search completed: October 27, 2003, 12:03:09
Job time : 178.849 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:53:10 ; Search time 43 4627 Seconds
(without alignments)
5910.475 Million cell updates/sec

Title: US-09-925-674A-8
Perfect score: 582
Sequence: 1 atggcgagccagctcaac.....cctttttgtagcaactga 582

Scoring table: IDENTITY NJC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 3
Maximum DB seq length: 2500000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:
5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558.2	95.9	579	1	US-08-798-897-1
2	558.2	95.9	579	2	US-08-978-523-1
3	515	88.5	579	1	US-08-798-897-2
4	515	88.5	579	2	US-08-978-523-2
5	372.4	64.0	1864	4	US-09-149-476-130
6	134.6	23.1	926	1	US-08-081-448-5
7	134.6	23.1	926	2	US-08-470-670A-6
8	134.6	23.1	926	3	US-08-481-739-1
9	134.6	23.1	926	3	US-09-167-921-1
10	134.6	23.1	926	3	US-09-277-020-39
11	134.6	23.1	926	3	US-09-323-743-1
12	134.6	23.1	926	4	US-08-461-511A-6
13	134.6	23.1	926	4	US-09-271-014A-5
14	134.6	23.1	926	5	PCT-US94-07089-6
15	121.8	20.9	717	2	US-08-465-485A-20
16	121.8	20.9	717	3	US-09-080-285-20
17	121.8	20.9	1274	2	US-08-470-670A-1
18	121.8	20.9	1274	4	US-08-461-511A-1
19	121.8	20.9	1274	5	PCT-US94-07089-1
20	121.8	20.9	1303	1	US-08-081-448-1
21	121.8	20.9	1303	4	US-09-271-014A-1
22	121.8	20.9	4825	6	5459251-1
23	121.8	20.9	5086	2	US-08-465-485A-19
24	121.8	20.9	5086	2	US-08-365-486A-14
25	121.8	20.9	5086	3	US-09-080-285-19
26	121.8	20.9	5086	3	US-08-880-342-14
27	121.8	20.9	5086	4	US-09-724-426-19

28	121.8	20.9	5086	4	US-09-233-527-7	Sequence 7, Appl 1
29	121.8	20.9	5086	5	PCT-US93-05651-4	Sequence 4, Appl 1
30	121.8	20.9	5086	5	PCT-US93-06251-2	Sequence 2, Appl 1
31	121.8	20.9	5094	4	US-09-234-186-7	Sequence 7, Appl 1
32	121.8	20.9	5104	6	5506344-1	Patent No. 5506344
33	120.2	20.7	760	1	US-08-405-702A-11	Sequence 11, Appl 1
34	120.2	20.7	1846	2	US-08-365-486A-16	Sequence 16, Appl 1
35	120.2	20.7	1846	2	US-08-880-342-16	Sequence 16, Appl 1
36	117.4	20.2	615	2	US-08-465-485A-22	Sequence 22, Appl 1
37	117.4	20.2	615	3	US-09-080-285-22	Sequence 22, Appl 1
38	117.4	20.2	911	3	US-09-126-109-5	Sequence 5, Appl 1
39	117.4	20.2	911	5	PCT-US93-06251-3	Sequence 3, Appl 1
40	115.6	19.9	1384	4	US-08-899-367-1	Sequence 1, Appl 1
41	114.2	19.6	831	6	5459251-3	Patent No. 5459251
42	114.2	19.6	831	6	5506344-4	Patent No. 5506344
43	73.2	12.6	623	6	5506344-3	Patent No. 5506344
44	57	9.8	737	1	US-08-081-448-7	Sequence 7, Appl 1
45	57	9.8	737	2	US-08-470-670A-8	Sequence 8, Appl 1

ALIGNMENTS

RESULT 1
US-08-798-897-1
: Sequence 1, Application US/08798897
: Patent No. 5789201
: GENERAL INFORMATION:
: APPLICANT: Guastella, John
: TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
: TITLE OF INVENTION: Homologue
: NUMBER OF SEQUENCES: 53
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
: STREET: 1100 New York Avenue, N.W., Suite 600
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20035
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.3C
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/798,897
: FILING DATE: February 11, 1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Esmond, Robert W.
: REGISTRATION NUMBER: 32,893
: REFERENCE/DOCKET NUMBER: 1483.0140001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 579 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: both
: MOLECULE TYPE: cDNA
US-08-798-897-1

Query Match	95.9%	Score 558.2;	DB 1;	Length 579;
Best Local Similarity	97.8%	Pred. No. 4.9e-143;		
Matches 566;	Conservative	0;	Mismatches 13;	Indels 0;
Gaps	0;			
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D5	1	ATGGCGACCCCGCTCAACCCCGACACACCGGGCTCTAGTGGCTGACTTTAGGCTAT	60	
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-08-978-523-1

Query Match 95.9%; Score 558.2; DB 2; Length 579;
Best Local Similarity 97.8%; Pred. No. 4.9e-143;
Matches 566; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Dd : ATGGGACCCAGCCCTCAACCCACAGACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
QY 61 AGGCTGAGGACAGAGGGTTATGCTGTGGAGCTGCCCTGGGGAAGGCCAGCCGCCGAC 120
Dd 61 AGGCTGAGGACAGAGGGTTATGCTGTGGAGCTGCCCTGGGGAAGGCCAGCCGCCGAC 120
QY 121 CCGCTGCACCAAGCCATCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCGCCGCCACC 180
Dd 121 CCGCTGCACCAAGCCATCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCGCCGCCACC 180
QY 181 TTCTCTGACCTGGCCGCTCAGCTACAGTACAGCCAGGCTCAGCCAGCAAGGCTTCACC 240
Dd 181 TTCTCTGACCTGGCCGCTCAGCTACAGTACAGCCAGGCTCAGCCAGCAAGGCTTCACC 240
QY 241 CAGGTTTCCGAGCAACTTTTCCAAAGGGGGCCCTTAAGTGGGGCCGCTTGTGGCAATCTTT 300
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Dd 301 GTCTTTGGGGCTGCCCTGTGTGCTCAGAGTGTCAACAAAGAAATGAGAGCTTTGTGGGA 360
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Dd 361 CAAGTGCAGGATTGGATGGTGGCTTACAGCTCTATACGGGACGGGCCCTGGAGGAGGACGG 420
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Dd 421 AGTGGCGCTGGCGGAGTTACAGCTCTATACGGGACGGGGCCCTGGAGGAGGACGG 480
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Dd 481 CGTCTGGGAGGGGAACCTGGGCATCAGTAGGACAGTGCCTGACGGGGGCCCTGGCACTG 540
QY 541 GGGGCCCTGCTAACTGTAGGGGCCCTTTTGTGCTAGCAAG 579
Dd 541 GGGGCCCTGCTAACTGTAGGGGCCCTTTTGTGCTAGCAAG 579
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RESULT 2

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US-08-978-523-1
; Sequence 1, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1463.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-08-978-523-1

Query Match 95.9%; Score 558.2; DB 2; Length 579;
Best Local Similarity 97.8%; Pred. No. 4.9e-143;
Matches 566; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATGGGACCCAGCCCTCAACCCACAGACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Dd : ATGGGACCCAGCCCTCAACCCACAGACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
QY 61 AGGCTGAGGACAGAGGGTTATGCTGTGGAGCTGCCCTGGGGAAGGCCAGCCGCCGAC 120
Dd 61 AGGCTGAGGACAGAGGGTTATGCTGTGGAGCTGCCCTGGGGAAGGCCAGCCGCCGAC 120
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Dd 121 CCGCTGCACCAAGCCATCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCGCCGCCACC 180
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Dd 181 TTCTCTGACCTGGCCGCTCAGCTACAGTACAGCCAGGCTCAGCCAGCAAGGCTTCACC 240
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Dd 361 CAAGTGCAGGATTGGATGGTGGCTTACAGCTCTATACGGGACGGGCCCTGGAGGAGGACGG 420
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Dd 421 AGTGGCGCTGGCGGAGTTACAGCTCTATACGGGACGGGGCCCTGGAGGAGGACGG 480
QY 481 CGTCTGGGAGGGGAACCTGGGCATCAGTAGGACAGTGCCTGACGGGGGCCCTGGCACTG 540
Dd 481 CGTCTGGGAGGGGAACCTGGGCATCAGTAGGACAGTGCCTGACGGGGGCCCTGGCACTG 540
QY 541 GGGGCCCTGCTAACTGTAGGGGCCCTTTTGTGCTAGCAAG 579
Dd 541 GGGGCCCTGCTAACTGTAGGGGCCCTTTTGTGCTAGCAAG 579
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RESULT 3

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US-08-798-897-2
; Sequence 2, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-08-798-897-2

Query Match      88.5%; Score 515; DB 1; Length 579;
Best Local Similarity 93.1%; Pred. No. 2.9e-131;
Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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DB 1 ATGGGACCCAGCCTCGGCCCCAGACACACAGGGCTCTGGTGGAAAGACTTTGTAGGTTAT 60
QY 61 AGGCTGAGGACAGAGGGTTATGCTGTGGAGTGGCCCTGGGGAAGGCCACGCCGCCAC 120
DB 61 AAGCTGAGGACAGAGGGTTATGCTGTGGAGTGGCCCGGGGGAGGCCACGAGTGAC 120
QY 121 CCGCTGCACCAAGCCATCGGGCTCTGGAGACGAGTTTGAGACCGGTTTCGGCGGCACC 180
DB 121 CCACCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGCGGCACC 180
QY 181 TTCTCTGACTGGCCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
DB 181 TTCTCTGATCTGGCGCTCAGCTGATGTGACCCAGGCTCAGCCCAACAGCCTTCACC 240
QY 241 CAGGTTCCGACAACTTTTCCAAAGGGGCCCTAACTGGGGCCGCTCTGTGTGGCAATCTTT 300
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QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATCGAGCCTTTGGTGGGA 360
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QY 361 CAAGTGCAGATTGGATGGTGGCTTACCTGGAGACACAGCTCTGGCTGACTGATCCACAGC 420
DB 361 CAAGTGCAGAGTGGATGGTGGCTTACCTGGAGAGACGGGCTGGCTGACTGATCCACAGC 420
QY 421 AGTGGCGGCTGGGCGGAGTTTACAGCTCTATACGGGGACGGGGCCCTGGAGGAGCACGG 480
DB 421 AGTGGGGGCTGGGCGGAGTTTACAGCTCTATACGGGGACGGGGCCCTGGAGGAGCGCGG 480
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RESULT 4
US-08-978-523-2
; Sequence 2, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
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; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-08-978-523-2

Query Match      88.5%; Score 515; DB 2; Length 579;
Best Local Similarity 93.1%; Pred. No. 2.9e-131;
Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 ATGGGACCCAGCCTCAACCCAGACACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
DB 1 ATGGGACCCAGCCTCGGCCCCAGACACACAGGGCTCTGGTGGAAAGACTTTGTAGGTTAT 60
QY 61 AGGCTGAGGACAGAGGGTTATGCTGTGGAGTGGCCCTGGGGAAGGCCACGCCGCCAC 120
DB 61 AAGCTGAGGACAGAGGGTTATGCTGTGGAGTGGCCCGGGGGAGGCCACGAGTGAC 120
QY 121 CCGCTGCACCAAGCCATCGGGCTCTGGAGACGAGTTTGAGACCGGTTTCGGCGGCACC 180
DB 121 CCACCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGCGGCACC 180
QY 181 TTCTCTGACTGGCCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
DB 181 TTCTCTGATCTGGCGCTCAGCTGATGTGACCCAGGCTCAGCCCAACAGCCTTCACC 240
QY 241 CAGGTTCCGACAACTTTTCCAAAGGGGCCCTAACTGGGGCCGCTCTGTGTGGCAATCTTT 300
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QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATCGAGCCTTTGGTGGGA 360
DB 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360
QY 361 CAAGTGCAGATTGGATGGTGGCTTACCTGGAGACACAGCTCTGGCTGACTGATCCACAGC 420
DB 361 CAAGTGCAGAGTGGATGGTGGCTTACCTGGAGAGACGGGCTGGCTGACTGATCCACAGC 420
QY 421 AGTGGCGGCTGGGCGGAGTTTACAGCTCTATACGGGGACGGGGCCCTGGAGGAGCACGG 480
DB 421 AGTGGGGGCTGGGCGGAGTTTACAGCTCTATACGGGGACGGGGCCCTGGAGGAGCGCGG 480
QY 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTGTCTAGCAAG 579
DB 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTGTCTAGCAAG 579
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Qy 481 CGTCTGGGAGGGAACTGGGCATCAGTCAGGACACTGCTGACGGGGGCCGTGGCACTG 540
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481 CGTCTGGGAGGGAACTGGGCATCAGTCAGGACACTGCTGACGGGGGCCGTGGCACTG 540
Qy 541 GGGGCCCTGCTACTGTAGGGGCTTTTTCCTAGCAAG 579
Db [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
541 GGGGCCCTGCTACTGTAGGGGCTTTTTCCTAGCAAG 579

RESULT 5
US-09-149-476-130
; Sequence 130, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
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; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
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; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
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; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
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; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22

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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 64.0%; Score 372.4; DB 4; Length 1864;
Best Local Similarity 91.2%; Pred. No. 3.1e-92;
Matches 394; Conservative 1; Mismatches 37; Indels 0; Gaps 0;
1 ATGGCGACCCAGCTCAGCCAGACACACAGCGGCTCTAGTGGTGAATTTGTAGGCTAT 60
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DB 11 ATGGCGACCCAGCTCAGCCAGACACACAGCGGCTCTGGTGGCAGACTTTGTAGGTTAT 70
QY 61 AGGTGAGGCAGAAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGCCAGCCGCGAC 120
DB 71 AAGCTGAGGCAGAAAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 130
QY 121 CCGTGCACCAAGGCATGCGGGCTGCTGGAGACAGTTTGGAGCCCGTTTCCGCGCGACC 180
DB 131 CCGTGCACCAAGGCATGCGGGCGAGCKGAGATGAGTTGAGAGCCCGCTTCCGCGCGACC 190
QY 181 TTCTCTGACCTGGCGGCTCAGCTACAGCTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
DB 191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACAGGCTTCACC 250
QY 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCTTAACCTGGGGCCCTTTGTGGGCAATCTTT 300
DB 251 CAGGCTCTCCGATGAATTTTCAAGGGGCGCCCACTGGGGCGCGCTTGTAGCCTCTTT 310
QY 301 GTCTTGGGGCTGCCCTGTGTGTGAGAGTGTCAACAAGAAATGGAGCCCTTGTGGGA 360
DB 311 GTCTTGGGGCTGCACCTGTGTGTGAGAGTGTCAACAAGAGATGGAAACCACTGTGGGA 370
QY 361 CAAGTCAGGATTTGATGTTGGGCTTACCTGGAGACAGTCTGGCTGACTGGATCCAGC 420
DB 371 CAAGTCAGGATTTGATGTTGGGCTTACCTGGAGACAGGCTGGCTGACTGGATCCAGC 430
QY 421 AGTGGCGCTCG 432
DB 431 AGTGGCGCTCG 442
RESULT 6
US-08-081-448-5
Sequence 5, Application US/08081448
Patent No. 5646008
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5646008th Clark Street, Suite 800
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,448
FILING DATE: 19930622
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646008thrup, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
TELEFAX: 312-755-4489
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS

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; LOCATION: 135...836
; US-08-081-448-5

Query Match      23.1%; Score 134.6; DB 1; Length 926;
Best Local Similarity 58.3%; Pred. No. 1.6e-27;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCATGCGGCTGCTGGAGAGAGTTTGGAGACCGGTTTCCGCGGACCTTCTCTG 187
DB 394 AGCAAGCGCTGAGGGAGGCGAGCGAGGTTTGAACCTGCGGTACCGGGGCGATTCACTG 453
QY 188 ACCTGGCCGCTCAGTACACGTGACCCCGAGGCTCAGCCCGAGCAACGCTTACCAGGTTT 247
DB 454 ACCTGACATCCAGCTCCACATCACCAGGAGCATATCAGAGCTTTGAACAGGTAG 513
QY 248 CCGACGAACCTTTCCAGGGGGCCCTAACTGGGGCGGCTTGGAGACCGGTTTCCGCGGACCTTCTCTG 307
DB 514 TGAATGAACCTTTCCGAGATGGGTAACTGGGTGCGCATTTGGCCCTTTTCTCTCTG 573
QY 308 GGGCTGCCCTGTGTGAGAGTGTCAACAAAGAAATGGAGCCCTTTGGTGGCAAGTGC 367
DB 574 GCGGGGCACTGTGGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGGATCG 633
QY 368 AGGATTGATGGTGGCTTACAGCTCTATACGGGAGCGGGCCCTGGAGGAGCGACGGCGTCTGC 427
DB 634 CAGCTTGGATGGCACTTACTCTGAATGACCACTAGAGCCTTGGATCCAGGAGACGGCG 693
QY 428 GCTGGCGGAGTTTCAAGCTTATAGCGGAGCGGGCCCTGGAGGAGCGACGGCGTCTGC 487
DB 694 GCTGGGATCTTTTGTGAACTCTATGGAAACAAATGCAGCAGCGAGAGCGAAAGGGCC 753
QY 488 GGGAGGGAACTGGGCACTCAGTGAGGACAGTGTGACGGGGCGG 532
DB 754 AGGAACGCTTCAACCGCTGGTTCTCTGACGGGCGATGACTGTGGCGG 798

RESULT 7
US-08-470-670A-6
; Sequence 6, Application US/08470670A
; Patent No. 5834309
; Patent No. 5834309 5710045
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B. B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,670A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,448
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:090--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135...836
; US-08-470-670A-6

Query Match      23.1%; Score 134.6; DB 2; Length 926;
Best Local Similarity 58.3%; Pred. No. 1.6e-27;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCATGCGGCTGCTGGAGAGAGTTTGGAGACCGGTTTCCGCGGACCTTCTCTG 187
DB 394 AGCAAGCGCTGAGGGAGGCGAGCGAGGTTTGAACCTGCGGTACCGGGGCGATTCACTG 453
QY 188 ACCTGGCCGCTCAGTACACGTGACCCCGAGGCTCAGCCCGAGCAACGCTTACCAGGTTT 247
DB 454 ACCTGACATCCAGCTCCACATCACCAGGAGCATATCAGAGCTTTGAACAGGTAG 513
QY 248 CCGACGAACCTTTCCAGGGGGCCCTAACTGGGGCGGCTTGGAGACCGGTTTCCGCGGACCTTCTCTG 307
DB 514 TGAATGAACCTTTCCGAGATGGGTAACTGGGTGCGCATTTGGCCCTTTTCTCTCTG 573
QY 308 GGGCTGCCCTGTGTGAGAGTGTCAACAAAGAAATGGAGCCCTTTGGTGGCAAGTGC 367
DB 574 GCGGGGCACTGTGGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGGATCG 633
QY 368 AGGATTGATGGTGGCTTACAGCTCTATACGGGAGCGGGCCCTGGAGGAGCGACGGCGTCTGC 427
DB 634 CAGCTTGGATGGCACTTACTCTGAATGACCACTAGAGCCTTGGATCCAGGAGACGGCG 693
QY 428 GCTGGCGGAGTTTCAAGCTTATAGCGGAGCGGGCCCTGGAGGAGCGACGGCGTCTGC 487
DB 694 GCTGGGATCTTTTGTGAACTCTATGGAAACAAATGCAGCAGCGAGAGCGAAAGGGCC 753
QY 488 GGGAGGGAACTGGGCACTCAGTGAGGACAGTGTGACGGGGCGG 532
DB 754 AGGAACGCTTCAACCGCTGGTTCTCTGACGGGCGATGACTGTGGCGG 798

RESULT 8
US-08-481-739-1
; Sequence 1, Application US/08481739
; Patent No. 6143291
; GENERAL INFORMATION:
; APPLICANT: June, Carl H. and Thompson, Craig B.
; TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
; TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,739
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,518
; FILING DATE: 04-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. (GAD)
```

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; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RPI-034CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nuc.eic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; US-08-481-739-1

Query Match      23.1%; Score 134.6; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 1.6e-27;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGCTGCTGAGACGAGTTTGAGACCCGTTTCGCGCGACGCTTCTCTG 187
DB 394 AGCAAGCGCTGAGGAGGCGACGAGTTTGAACCTGCGGTACCGCGCGGCGATTTCAGTG 453

QY 188 ACCTGGCGCTCAGCTACAGTGCACCCAGGCTGACCCAGGCTGACCCAGCAACGCTTCACCCAGGTTT 247
DB 454 ACCTGACATCCCGAGCTCCACATCAACCCAGGAGCAGCATATCAGAGCTTTGAACAGGTTAG 513

QY 248 CCGACGAACCTTTTCAAGGGGGCCCTAACTGGGGCGCTTCTGTGGCATCTTTTGTCTTTG 307
DB 514 TGAATGAACCTTTCCGGGATGGGTAACTGGGTGCGATTGCGCTTTTCTCTCTCG 573

QY 308 GGGCTGCCCTGTGCTGAGAGTGTCAACAAGAAATGAGGCTTTGTGGGACAAGTGC 367
DB 574 GCGGGCACTGTCGGTGAAGAGGTAGACAAGGAGATGCAAGTATTGGTGAGTCGATCG 633

QY 368 AGGATTGGATGCTGGCTACCTGGAGACAGCTTCTGCTGACTGGATCCACAGCAGTGGCG 427
DB 634 CAGCTTGGATGGCCACTTACCTGGAATGACCACCTAGAGCTTGGATCCAGGAGAACGGCG 693

QY 428 GCTGGCGGAGTTTCACAGCTCTATACGGGGACGGGGCCCTGGAGAGGACGCGGCTCTGC 487
DB 694 GCTGGGATCTTTTGTGGAACCTCTATGGGAACTATGGGAACTATGGGAGCCGAGAGCGCC 753

QY 488 GGGAGGGAACTGGGCACTGAGGACAGTGTGAGGAGGAGTGTGAGGGGGCGG 532
DB 754 AGGAACGCTTCAACCGCTGTTCTCTGACGGGCATGACTGTGGCGG 798

RESULT 9
US-09-167-921-1
; Sequence 1, Application US/09167921A
; Patent No. 6172216
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0324
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (135)..(836)

; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RPI-034CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nuc.eic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; US-08-481-739-1

Query Match      23.1%; Score 134.6; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 1.6e-27;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGCTGCTGAGACGAGTTTGAGACCCGTTTCGCGCGACGCTTCTCTG 187
DB 394 AGCAAGCGCTGAGGAGGCGACGAGTTTGAACCTGCGGTACCGCGCGGCGATTTCAGTG 453

QY 188 ACCTGGCGCTCAGCTACAGTGCACCCAGGCTGACCCAGGCTGACCCAGCAACGCTTCACCCAGGTTT 247
DB 454 ACCTGACATCCCGAGCTCCACATCAACCCAGGAGCAGCATATCAGAGCTTTGAACAGGTTAG 513

QY 248 CCGACGAACCTTTTCAAGGGGGCCCTAACTGGGGCGCTTCTGTGGCATCTTTTGTCTTTG 307
DB 514 TGAATGAACCTTTCCGGGATGGGTAACTGGGTGCGATTGCGCTTTTCTCTCTCG 573

QY 308 GGGCTGCCCTGTGCTGAGAGTGTCAACAAGAAATGAGGCTTTGTGGGACAAGTGC 367
DB 574 GCGGGCACTGTCGGTGAAGAGGTAGACAAGGAGATGCAAGTATTGGTGAGTCGATCG 633

QY 368 AGGATTGGATGCTGGCTACCTGGAGACAGCTTCTGCTGACTGGATCCACAGCAGTGGCG 427
DB 634 CAGCTTGGATGGCCACTTACCTGGAATGACCACCTAGAGCTTGGATCCAGGAGAACGGCG 693

QY 428 GCTGGCGGAGTTTCACAGCTCTATACGGGGACGGGGCCCTGGAGAGGACGCGGCTCTGC 487
DB 694 GCTGGGATCTTTTGTGGAACCTCTATGGGAACTATGGGAACTATGGGAGCCGAGAGCGCC 753

QY 488 GGGAGGGAACTGGGCACTGAGGACAGTGTGAGGAGGAGTGTGAGGGGGCGG 532
DB 754 AGGAACGCTTCAACCGCTGTTCTCTGACGGGCATGACTGTGGCGG 798

RESULT 10
US-09-277-020-39
; Sequence 39, Application US/09277020
; Patent No. 6210892
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
; FILE REFERENCE: ISPH-0339
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: US/09/277,020
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (135)..(836)

; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RPI-034CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nuc.eic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; US-08-481-739-1

Query Match      23.1%; Score 134.6; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 1.6e-27;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGCTGCTGAGACGAGTTTGAGACCCGTTTCGCGCGACGCTTCTCTG 187
DB 394 AGCAAGCGCTGAGGAGGCGACGAGTTTGAACCTGCGGTACCGCGCGGCGATTTCAGTG 453

QY 188 ACCTGGCGCTCAGCTACAGTGCACCCAGGCTGACCCAGGCTGACCCAGCAACGCTTCACCCAGGTTT 247
DB 454 ACCTGACATCCCGAGCTCCACATCAACCCAGGAGCAGCATATCAGAGCTTTGAACAGGTTAG 513

QY 248 CCGACGAACCTTTTCAAGGGGGCCCTAACTGGGGCGCTTCTGTGGCATCTTTTGTCTTTG 307
DB 514 TGAATGAACCTTTCCGGGATGGGTAACTGGGTGCGATTGCGCTTTTCTCTCTCG 573

QY 308 GGGCTGCCCTGTGCTGAGAGTGTCAACAAGAAATGAGGCTTTGTGGGACAAGTGC 367
DB 574 GCGGGCACTGTCGGTGAAGAGGTAGACAAGGAGATGCAAGTATTGGTGAGTCGATCG 633

QY 368 AGGATTGGATGCTGGCTACCTGGAGACAGCTTCTGCTGACTGGATCCACAGCAGTGGCG 427
DB 634 CAGCTTGGATGGCCACTTACCTGGAATGACCACCTAGAGCTTGGATCCAGGAGAACGGCG 693

QY 428 GCTGGCGGAGTTTCACAGCTCTATACGGGGACGGGGCCCTGGAGAGGACGCGGCTCTGC 487
DB 694 GCTGGGATCTTTTGTGGAACCTCTATGGGAACTATGGGAACTATGGGAGCCGAGAGCGCC 753

QY 488 GGGAGGGAACTGGGCACTGAGGACAGTGTGAGGAGGAGTGTGAGGGGGCGG 532
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RESULT 11
US-09-277-020-39
; Sequence 39, Application US/09277020
; Patent No. 6210892
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
; FILE REFERENCE: ISPH-0339
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: US/09/277,020
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (135)..(836)
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Db 514 TGATGAACCTCTCCGGGATGGGTAAACTGGGGTCCACTTTTCTCTCTCG 573
Qy 308 GGGCTGGCCTGTGTCCTGAGAGTGTCAACAAAGAAATGAGCCCTTTGGTGGGACAAAGTGC 367
Db 574 GCGGGGCACTGTGGTGGAAAGCGTACACAGAGAGATGCAGGTATTGGTGAGTGGATCG 633
Qy 368 AGGATTGGATGGTGGCTACTCTGAGACACAGTCTGGTGTGACTGATCCACAGSAGTGGCG 427
Db 634 CAGCTTGATGGCCCACTTACCTGAATGACCACTAGAGCCTTGGATCCAGGAGAACGGCG 693
Qy 428 GCTGGCGGAGTTCACAGCTCTATACGGGACGGGCCCTGGAGGAGCGACGGCTCTGC 487
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Qy 488 GGGAGGGAACCTGGGCACTCAGTAGGACAGTGTCTGACGGGGCGG 532
Db 754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCG 798
RESULT 11
US-09-323-743-1
; Sequence 1, Application US/09323743
; Patent No. 6214986
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QiangQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISFH-0368
; CURRENT APPLICATION NUMBER: US/09/323,743
; CURRENT FILING DATE: 1999-06-01
; EARLIER APPLICATION NUMBER: 09/277,020
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 09/167,921
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135...836)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
US-09-323-743-1
Query Match 23.1%; Score 134.6; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 1.6e-27;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
Qy 128 ACCAAGCCATCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCGGCGGACCTTCTCTG 187
Db 394 AGCAAGCGCTGAGGAGGACGGGACGAGTTGAACTGGGTACCGGGCGGCAATTCAGTG 453
Qy 188 ACCTGGCGGCTCAGCTACACGTGACCCGAGGCTCAGCCGAGCAACGCTTACCCAGGTTT 247
Db 454 ACCTGACATCCAGCTCCACATACCCGAGGACAGCATATCAGAGCTTGNACAGGTAG 513
Qy 248 CCGACGAACATTTTCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATCTCTTGTCTTG 307
Db 514 TGAATGAACCTCTCCGGGATGGGTAAACTGGGGTGGCATTTGGCCCTTTTCTCTCTCG 573
Qy 368 AGGATTGGATGGTGGCTTACCTGGAGACAGCTCTGGCTGACTGGATCCACAGAGTGGCG 427

Db 634 CAGCTTGATGGCCACTTACCTGAATGACACCTAGAGCCTTGGATCCAGGAGAACGGCG 693
Qy 428 GCTGGCGGAGTTCACAGCTCTATACGGGACGGGCCCTTGAGGAGGACACGGGCTCTGC 487
Db 694 GCTGGGATACTTTTGTGGAACCTTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 753
Qy 488 GGGAGGGAACCTGGGCACTCAGTAGGACAGTGTCTGACGGGGGGCG 532
Db 754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCG 798
RESULT 12
US-08-461-511A-6
; Sequence 6, Application US/08461511A
; Patent No. 6303331
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
; AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,511A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: UNKNOWN
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-461-511A-6
Query Match 23.1%; Score 134.6; DB 4; Length 926;
Best Local Similarity 58.3%; Pred. No. 1.6e-27;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
Qy 128 ACCAAGCCATCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCGGCGGACCTTCTCTG 187
Db 394 AGCAAGCGCTGAGGAGGACGGGACGAGTTGAACTGGGTACCGGGCGGCAATTCAGTG 453
Qy 188 ACCTGGCGGCTCAGCTACACGTGACCCGAGGCTCAGCCGAGCAACGCTTACCCAGGTTT 247
Db 454 ACCTGACATCCAGCTCCACATACCCGAGGACAGCATATCAGAGCTTGNACAGGTAG 513
Qy 248 CCGACGAACATTTTCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATCTCTTGTCTTG 307
Db 514 TGAATGAACCTCTCCGGGATGGGTAAACTGGGGTGGCATTTGGCCCTTTTCTCTCTCG 573
Qy 308 GGGCTGGCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGGGACAAAGTGC 367

Db 574 CGGGGACCTGTGCTGGAAGCGTAGCAGAGGATGCGAGTATTGGTAGTCGATCG 633
Qy 368 AGGATTGGATGGTGGCTTACCTGAGACACGCTCTGGCTGACTGGATCCACAGCAGTGGCG 427
Db 634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCCTTGGATCCAGGAGAACGGCG 693
Qy 428 GCTGGGCGGAGTTCACAGCTCTATACGGGACGGGCGCTTGGAGGAGGACGGGCTGTC 487
Db 694 GCTGGGATACTTTGTGGAATCTATGGAACCAATGACAGCGCGAGCGGAAAGGGCC 753
Qy 488 GGGAGGGGAACCTGGGCACTCAGTAGGACAGCTGTGACGGGGCGG 532
Db 754 AGGACGCTTCAACCGCTGGTTCCTGACGGCATGACTGTGGCG 798

RESULT 13
US-09-271-014A-5
; Sequence 5, Application US/09277:014A
; Patent No. 6395510
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, CRAIG B.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD.316
; CURRENT APPLICATION NUMBER: US/09/271.014A
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(836);
US-09-271-014A-5

Query Match 23.1%; Score 134.6; DB 4; Length 926;
Best Local Similarity 58.3%; Pred. No. 1.6e-27;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

Qy 128 ACCAAGCATCGGGCTGCTGGAGCAGAGTTTGAGCCGTTTCGGCGGACCTTCTCTG 187
Db 394 AGCAGCGCTGAGGAGGACGAGCGACAGTTTGAACCTGCGTACCGGGGCACTCAGTG 453
Qy 188 ACCTGGCGCTCAGCTACACGTGACCCAGGCTCAGCCCAAGCAACGCTTCAACCAAGTTT 247
Db 454 ACCTGACATCCAGCTCCACATCACCAGGACAGCATATCAGAGCTTTGAACAGGTAG 513
Qy 248 CCGAGCAACTTTTCAAGGGGCGCTTAACCTGGGTCGCAATTTGGCCCTTTTCTCCTTCG 307
Db 514 TGAATGAACTCTTCGGGATGGGTAACCTGGGTCGCAATTTGGCCCTTTTCTCCTTCG 573
Qy 308 GGGCTGCCCTGTGTCTCAGAGTGTCAACAAAGAAATGGAGCCCTTTGGTGGACAAGTGC 367
Db 574 GCGGGCACTGTGCTGGAAGCGGTAGACAAGAGATGAGGTATTGGTAGTCGATCG 633
Qy 368 AGGATTGGATGGTGGCTTACCTGGAGACACGCTGTGGCTGACTGGATCCACAGCAGTGGCG 427
Db 634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCCTTGGATCCAGGAGAACGGCG 693
Qy 428 GCTGGGCGGATTCACAGCTCTATACGGGACGGGCGCTTGGAGGAGGACGGGCTGTC 487
Db 694 GCTGGGATACTTTGTGGAATCTATGGAACCAATGACAGCAGCGGAGCGGAAAGGGCC 753
Qy 488 GGGAGGGGAACCTGGGCATCAGTAGGACAGTGTGACGGGGCGG 532
Db 754 AGGAAAGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCGG 798

RESULT 14
PCT-US94-07089-6

; Sequence 6, Application PC/TUS9407089
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07089
; FILING DATE: CONCURRENTLY FILED
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/081.448
; FILING DATE: 22 JUNE 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; PCT-US94-07089-6

Query Match 23.1%; Score 134.6; DB 5; Length 926;
Best Local Similarity 58.3%; Pred. No. 1.6e-27;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

Qy 128 ACCAAGCATCGGGCTGCTGGAGCAGAGTTTGAGACCGGTTTCGGCGGACCTTCTCTG 187
Db 394 AGCAAGCGCTGAGGAGGCGAGCGAGTGTGAACTGCGGTACCGGGGCACTCAGTG 453
Qy 188 ACCTGGCGCTCAGCTACAGTGACCCAGGCTCAGCCCAAGCAACGCTTCAACCAAGTTT 247
Db 454 ACCTGACATCCAGCTCCACATCACCAGGAGACAGCATATCAGAGCTTTGAACAGGTAG 513
Qy 248 CCGACCAACTTTTCAAGGGGCGCTTAACCTGGGCGCTTGTGGCATCTTTGTCTTTG 307
Db 514 TGAATGAACTCTTCGGGATGGGTAACCTGGGTCGCAATTTGGCCCTTTTCTCCTTCG 573
Qy 308 GGGCTGCCCTGTGTCTGAGAGTGTCAACAAAGAAATGGAGCCCTTTGGTGGACAAGTGC 367
Db 574 GCGGGCACTGTGCTGGAAGCGGTAGACAAGAGATGAGGTATTGGTAGTCGATCG 633
Qy 368 AGGATTGGATGGTGGCTTACCTGGAGACACGCTGTGGCTGACTGGATCCACAGCAGTGGCG 427
Db 634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCCTTGGATCCAGGAGAACGGCG 693
Qy 428 GCTGGGCGGATTCACAGCTCTATACGGGACGGGCGCTTGGAGGAGGACGGGCTGTC 487
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Qy 488 GGGAGGGGAACCTGGGCATCAGTAGGACAGTGTGACGGGGCGG 532

Db 754 AGGAACGCTTCAACCGCTGGTCTCTGAGCGCATGACTGTGGCG 798

RESULT 15
US-08-465-485A-20
; Sequence 20, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; City: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 717 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..717
US-08-465-485A-20

Query Match 20.9%; Score 121.8; DB 2; Length 717;
Best Local Similarity 58.4%; Pred. No. 4.4e-24;
Matches 213; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

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QY 151 GACGAGTTGAGACCCGCTTCGCGCGCACCTCTCTGACCTGGCGCTCAGCTACAGTG 210
DB 304 GACGACTTCTCCCGCGGTACCGCGCGGACTTCGCGGAGATGTCCAGCCAGCTCACCCTG 363
QY 211 ACCCCAGGCTCAGCCAGCAAGCGTTTCCAGAGTTTCCGACGAACTTTTCCAAAGGGGC 270
DB 364 ACGCCCTTCAACCGCGGGGAGCGTTTGCACGCGTGGTGGAGGAGCTCTTCAGGGACGG 423
QY 271 CCTAACTGGGCGCTCTTGTGGCATCTTTTGTGGGCTGCCTGTGTGTGAGAGT 330

Db 424 GTGAACCTGGGGGAGGATTGTGGCCCTTCTTTGAGTTCCGGTGGGTCTATGTGTGGAGAGC 483
QY 331 GTCAACAAAGAAATGGAGCCCTTTGGTGGGACAAAGTGCAGGATTGGATGGTGGCCTTACCTG 390
Db 484 GTCAACCGGGAGATGTGGCCCTCTGGTGGACAAACATCGCCCTGTGGATGACTGAGTACCTG 543
QY 391 GAGACACGCTCTGGCTGACTGGATCCACAGCAGTGGCGGCTGGCGGAGTTTCACAGCTCTA 450
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QY 451 TACGG 455
Db 604 TACGG 608

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 13:01:31 ; Search time 162.361 Seconds
(without alignments)
9613.225 Million cell updates/sec

Title: US-09-925-674A-8

Perfect score: 582
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Scoring table: IDENTITY NJC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 134050451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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- 17: /cgn2_6/ptodata/1/pubpna/US06_PUBCOVB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	372.4	64.0	1864	12	US-09-882-171-130
5	372.2	64.0	578	12	US-10-029-386-10549
6	371.2	63.8	433	12	US-10-029-386-24249
7	218.6	37.6	6049	12	US-10-311-455-201
8	192.6	33.1	6049	12	US-10-311-455-202
9	149.4	25.7	151	12	US-10-029-386-27084
10	149.4	25.7	590	12	US-10-029-386-13384
11	148.4	25.5	150	9	US-09-864-761-17690
12	134.6	23.1	636	12	US-10-169-223-13
13	134.6	23.1	702	11	US-09-959-387-9
14	134.6	23.1	926	9	US-09-734-846-1
15	134.6	23.1	926	9	US-09-734-847A-39
16	134.6	23.1	926	10	US-09-922-278-5

17	134.6	23.1	926	12	US-10-302-262-1	Sequence 1, Appli
18	134.6	23.1	926	14	US-10-072-830-3	Sequence 3, Appli
19	126.8	21.8	600	9	US-09-864-761-7360	Sequence 3305, Ap
20	125.8	21.6	492	11	US-09-918-995-33305	Sequence 2481, A
21	125.8	21.6	555	9	US-09-864-761-24081	Sequence 20790, A
22	125.8	21.6	564	12	US-10-029-386-20790	Sequence 20, Appli
23	121.8	20.9	717	12	US-10-053-645A-20	Sequence 1, Appli
24	121.8	20.9	1350	14	US-10-072-830-1	Sequence 4, Appli
25	121.8	20.9	1303	10	US-09-952-278-1	Sequence 1, Appli
26	121.8	20.9	5086	8	US-08-726-211-4	Sequence 11, Appli
27	121.8	20.9	5086	12	US-10-141-618-11	Sequence 117, App
28	121.8	20.9	6030	12	US-10-007-926A-117	Sequence 187, App
29	121.8	20.9	6030	14	US-10-171-581-187	Sequence 13703, A
30	121.8	20.9	6142	14	US-10-198-846-13703	Sequence 22, Appli
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32	117.4	20.2	911	8	US-08-726-211-6	Sequence 912, App
33	115.6	19.9	1384	14	US-09-864-761-912	Sequence 199, App
34	94.4	16.2	439	9	US-09-864-761-912	Sequence 2435, Ap
35	77.4	13.3	6509	12	US-10-311-455-199	Sequence 28692, A
36	65	11.2	65	12	US-09-908-975-28692	Sequence 7, Appli
37	63.4	10.9	65	12	US-09-908-975-2435	Sequence 200, App
38	57	9.8	737	10	US-09-952-278-7	Sequence 20, Appli
39	56	9.6	6509	12	US-10-311-455-200	Sequence 20, Appli
40	47.6	8.2	5408	14	US-10-101-492-20	Sequence 20, Appli
41	42.8	7.4	867	12	US-10-140-472-20	Sequence 20, Appli
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43	42.8	7.4	867	12	US-10-142-885-20	Sequence 20, Appli
44	42.8	7.4	867	12	US-10-158-790-20	Sequence 20, Appli
45	42.8	7.4	867	14	US-10-123-155-20	Sequence 20, Appli

ALIGNMENTS

RESULT 1

US-09-925-674A-8
; Sequence 8, Application US/0925674A
; Patent No. US00020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(579)
US-09-925-674A-8

Query Match	100.0%	Score 582;	DB 10;	Length 582;
Best Local Similarity	100.0%	Pred. No. 2.8e-159;	Mismatches 0;	Indels 0;
Matches 582;	Conservative 0;	Indels 0;	Gaps 0;	
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DB	1	ATGGCAGCCAGCCTCAACCCAGACACACCGGGCTCTAGTGGCTGCTAGTGGCTAT	6C	
QY	61	AGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCCCTGGGAGGCCAGCCGCCGAC	12C	
DB	61	AGCTGAGGAGAGGGTTATGTCTGTGAGCTGGCCCTGGGAGGCCAGCCGCCGAC	12C	
QY	121	CCGCTGCACCAAGCCATCGGGCTGCTGGAGAGGAGTTTGGAGCCGTTTCCGCCGACC	18C	

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Db 121 CCGCTGACCAAGCCATCGCGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCGGCACC 180
Qy 181 TTCTCTGACCTGGCGGCTCAGCTACAGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
Db 181 TTCTCTGACCTGGCGGCTCAGCTACAGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
Qy 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTAACTGGGGCCGCTTTGTGGGATTCCTT 300
Db 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTAACTGGGGCCGCTTTGTGGGATTCCTT 300
Qy 301 GTCTTTGGGGCTGCCCTGTGCTGAGAGTGCTCAACAAGAAATGGAGGCTTTTGGTGGGA 360
Db 301 GTCTTTGGGGCTGCCCTGTGCTGAGAGTGCTCAACAAGAAATGGAGGCTTTTGGTGGGA 360
Qy 361 CAAGTGACAGGATTTGATGGGCTACCTGGAGACAGCTCTGGCTGACTGGATCCACAGC 420
Db 361 CAAGTGACAGGATTTGATGGGCTACCTGGAGACAGCTCTGGCTGACTGGATCCACAGC 420
Qy 421 AGTGGCGGCTGGCGGAGTTTCAAGCTCTATACGGGACGGGGCCCTGGAGGAGGACCGG 480
Db 421 AGTGGCGGCTGGCGGAGTTTCAAGCTCTATACGGGACGGGGCCCTGGAGGAGGACCGG 480
Qy 481 CGTCTGGGGAGGGGAACTGGGCACTCAGTGAGGACAGTGCTTGAGGGGGCGGTGGCACTG 540
Db 481 CGTCTGGGGAGGGGAACTGGGCACTCAGTGAGGACAGTGCTTGAGGGGGCGGTGGCACTG 540
Qy 541 GGGGCCCTGGTAACTGTAGGGGGCCCTTTTCTAGCAAGTGA 582
Db 541 GGGGCCCTGGTAACTGTAGGGGGCCCTTTTCTAGCAAGTGA 582
```

RESULT 2

```
US-09-925-674A-6
; Sequence 6, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN9965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 583
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(573)
US-09-925-674A-6
```

```
Query Match 90.1%; Score 524.4; DB 10; Length 583;
Best Local Similarity 93.8%; Pred. No. 1.5e-142;
Matches 546; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
```

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Qy 1 ATGGGACCCAGCCCTCAACCCAGACACAGGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db 1 ATGGGACCCAGCCCTCGGCCCCAGACACAGGGGCTCTGTGGCAGACTTTGTAGGTTAT 60
Qy 61 AGGCTGAGGCAAGAGGTTATGCTGTGAGCTGGCCCTGGGAGGCCAGCGCCGAC 120
Db 61 AAGCTGAGGCAAGAGGTTATGCTGTGAGCTGGCCCTGGGAGGCCAGCGCTGAC 120
Qy 121 CCGCTGCAACCAAGCCATCGGGCTGCTGGAGACGAGTTTGAGACCCGCTTCCGCGGCACC 180
Db 121 CCGCTGCAACCAAGCCATCGGGGAGCTGGAGATGAGTTTCGAGACCCGCTTCCGCGGCACC 180
```

```
Qy 181 TTCTCTGAGCTGGCGGCTCAGCTACAGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
Db 181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
Qy 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTAACTGGGGCCGCTTTGTGGCATTCTTT 300
Db 241 CAGGTTCTCGAGAACTTTTTCAGGGGGCCCAACTGGGGCCGCTTTGTAGCCTTCTTT 300
Qy 301 GTCTTTGGGGCTGCCCTGTGCTGAGAGTGCTCAACAAGAAATGGAGGCTTTTGGTGGGA 360
Db 301 GTCTTTGGGGCTGCCCTGTGCTGAGAGTGCTCAACAAGAGATGGAACCACTCGTGGGA 360
Qy 361 CAAGTGACAGGATTTGATGGGCTACCTGGAGACAGCTCTGGCTGACTGGATCCACAGC 420
Db 361 CAAGTGACAGGATTTGATGGGCTACCTGGAGACAGCTCTGGCTGACTGGATCCACAGC 420
Qy 421 AGTGGCGGCTGGCGGAGTTTCAAGCTCTATACGGGACGGGGCCCTGGAGGAGGACCGG 480
Db 421 AGTGGGGCTGGCGGAGTTTCAAGCTCTATACGGGACGGGGCCCTGGAGGAGGCGGG 480
Qy 481 CGTCTGGGGAGGGGAACTGGGCACTCAGTGAGGACAGTGCTTGAGGGGGCGGTGGCACTG 540
Db 481 CGTCTGGGGAGGGGAACTGGGCACTCAGTGAGGACAGTGCTTGAGGGGGCGGTGGCACTG 540
Qy 541 GGGGCCCTGGTAACTGTAGGGGGCCCTTTTCTAGCAAGTGA 582
Db 541 GGGGCCCTGGTAACTGTAGGGGGCCCTTTTCTAGCAAGTGA 582
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RESULT 3

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US-09-809-391-130
; Sequence 130, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1648)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-809-391-130
```

```
Query Match 64.0%; Score 372.4; DB 11; Length 1864;
Best Local Similarity 91.2%; Pred. No. 2.4e-98;
Matches 394; Conservative 1; Mismatches 37; Indels 0; Gaps 0;
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```
Qy 1 ATGGGACCCAGCCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db 11 ATGGGACCCAGCCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 70
Qy 61 AGGCTGAGGCAAGAGGTTATGCTGTGAGCTGGCCCTGGGGAGGCCAGCCGCGAC 120
Db 71 AAGCTGAGGCAAGAGGTTATGCTGTGAGCTGGCCCTGGGGAGGCCAGCGCTGAC 130
Qy 121 CCGCTGCAACCAAGCCATCGGGCTGCTGGAGACGAGTTTGAGACCCGCTTCCGCGCGCAC 180
Db 131 CCGCTGCAACCAAGCCATCGGGCAGCGKGGAGATGAGTTTCGAGACCGCTTCCGCGCGCAC 190
Qy 181 TTCTCTGAGCTGGCGGCTCAGCTACAGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
Db 191 TTCTCTGATCTGGCGGCTCAGCTGCAATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 250
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QY 1 ATGGCGACCCAGCGCTCAAA CCCCAGACACACGCGGCTCTAGTGGCTGACTTTGAGGCTAT 60
DB 105 ATGGCGACCCAGCGCTCGGCCCCAGACACACGCGCTCTGGTGGCAGACTTTGTAGGTTAT 164
QY 61 AGGCTGAGGCGAGAGGGTTATGTCGTGGAGCTGGCCCTGGGGAAGCCCGACGCGCGAC 120
DB 165 AAGCTGAGGCGAGAGGGTTATGTCGTGGAGCTGGCCCGGAGGCGCCAGCAGCTGAC 224
QY 121 CCGCTGCACCAAGCCATCGCGGCTGCTGGAGACGAGTTTGAGACCCGCTTTCCGCGCAC 180
DB 225 CCGCTGCACCAAGCCATCGCGGCACTGGAGATGAGTTTCGAGACCCGCTTCGCGCGAC 284
QY 181 TTCTCTGACCTGGCGGCTCAGCTACAGTACCCAGGCTCAGCCAGCAACGCTTCAC 240
DB 285 TTCTCTGATCTGGCGGCTCAGCTCATGTGACCCAGGCTCAGCCCAACACGCTTCAC 344
QY 241 CAGGTTTCCGACGAACTTTTCCAGGGGGGCGCTAACTGGGCGCTGTGTGGCATTTCTTT 320
DB 345 CAGGTTTCCGATGAACCTTTTCAAGGGGGGCGCCAACTGGGCGCGCTGTAGGCTTCTTT 404
QY 301 GTCTTTGGGCGTGGCGCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGGCGCTTTGGTGGGA 360
DB 405 GTCTTTGGGCGTGGCGCTGTGTGCTGAGAGTGTCAACAGGAGATGAGAACACTGGTGGGA 464
QY 361 CAAGTGACGAGATTGGATGGTGGCGCTCACTGGAGACAGTCTGGCTGACTGGATCCACAGC 420
DB 465 CAAGTGACGAGAGTGGATGGTGGCGCTCACTGGAGACGAGCTGGCTGACTGGATCCACAGC 524
QY 421 AGTGGCGGCTGGG 433
DB 525 AGTGGCGGCTGGG 537

RESULT 6
US-10-029-386-24249
; Sequence 24249, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Arnomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24249
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALU0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALU0.00e-72
; OTHER INFORMATION: NT HIT: G114751151, EVALU0.00e+00
US-10-029-386-24249

Cy	61	AGGCTGAGGCGAGAAAGGGTTATGTCTGTGAGAGCTGGCCCTGGGGAAGGCCCGCAGCGCGGAC	120
Db	62	AAAGCTGAGGCGAGAAAGGGTTATGTCTGTGAGAGCTGGCCCGGGGAGGGCCCGCAGCAGTGAC	121
Qy	121	CGGCTGCACCAAGCCATCGGGGCTGTCTGGAGACGAGTTTTCAGACCCGTTTCCGCCCGCAC	180
Db	122	CGGCTGCACCAAGCCATCGGGGAGCTGGAGATGAGTTTCAGACCCGCTTCGGGCGCAC	181
Qy	181	TTCTCTGAGCTGGCGGCTCAGCTACAGTGATGACCCAGGCTCAGCCCAAGCAAGCGTTTCAC	240
Db	182	TTCTCTGATCTGGCGGCTCAGCTGCAATGTGACCCAGGCTCAGCCCAAGCAAGCGTTTCAC	241
Qy	241	CAGGTTTCCGACGAACATTTTCCAAAGGGGGCCCTAACTGGGGCCGCTTTGTGGCAATCTTT	300
Db	242	CAGGTTTCCGATGAACATTTTCAAGGGGGCCCCAACTGGGGCCGCTTTGTAGCTCTTT	301
Qy	301	GTCTTTGGGCTGGCCCTGTGTCTGAGAGTGTCAACAAAGAAATGAGCGCTTTGGTGGGA	360
Db	302	GTCTTTGGGCTGGCACTGTGTCTGAGAGTGTCAACAAAGAGATGAACACCACCTGGTGGGA	361
Qy	361	CAAGTGCAGGATTTGATGGTGGCTACTCTGAGACAGCTGTGGCTGACTGGATCCACAGC	420
Db	362	CAAGTGCAGGAGTGGATGGTGGCTACTCTGAGACGAGCTGGCTGACTGGATCCACAGC	421
Qy	421	AGTGGCGCTGG 432	
Db	422	AGTGGCGCTGG 433	

```

RESULT 7
US-10-311-455-201
; Sequence 201, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: CLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 201
; LENGTH: 6049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens);
US-10-311-455-201

```

	Query Match	37.6%	Score 218.6	DB 12	Length 6049
	Best Local Similarity	69.1%	Pred. No. 1.3e-53		
	Matches 299	Conservative	0	Mismatches 134	Indels 0
Qy	1	ATGGCGACCCGAGCTCAACCCGACACACACGGGCTCTAGTGGCTGACTTTGTAGAGCTAT	60		
Db	5001	ATGGCGATTTTAGTTTCGGTTTTAGATATACGGGTTTTGGTGTAGATTTTGTAGGTTAT	5061		
Qy	61	AGGCTGAGGCACAAGGGTTATGCTCTGTGGAGCTGGCCCTGGGGAAGGCCACAGCCGCGAC	120		
Db	5061	AAGTTGAGGTAGAAGGGTTATGTTTGTGGAGTTCGTTTCGGGAGGGTTTAGTAGTTGAT	512		
Qy	121	CCGCTGCACAAAGCCATCGGGGCTCTCGGAGACGAGTTTGTAGACCCGCTTTCCGCGCGACC	180		
Db	5121	TGTTGTATTAAAGTTATCGGGGTAGTTGGAGATCAGATTCGAGATTTCGTTTCGCGGTATT	518		

QY 181 TTCTCTGACCTGGCCGCTCAGCTACAGTGCACCCAGCCGCTCAGCCAGCAACGCTTCACC 243
Db 5181 TTTTTCATTGGCGGTTAGTGTGTGTGATTTTAGGTTTAGTTTAATAACGTTTAT 5240
QY 241 CAGGTTTCCGACGAACTTTCCAGGGGGCCCTNACTGGGCGCTCTGTGGCATCTTT 353
Db 5241 TAGGTTTCGATGAATTTTTCAGGGGGTTTAAATGGGGGCTGTTTGTAGTTTITTT 5360
QY 301 GTCTTTGGGCGTGCCTGTGTCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 363
Db 5301 GTT-TTGGG-TGTAT-TGTGTGAGAG-TTAAAGGAGTGAATTA-TTGGTGGGA 5360
QY 361 CAAGTCAGGATTGGATGGTGGCCCTACTGGAGACAGTCTGGCTGACTGGATCCACAGC 420
Db 5361 TAAGTGTAGGAGTGGATGGTGGTTTATTTGGAGACGTAGTTGG-TGATTTGATTTATAGT 5420
QY 421 AGTGGCGCTGGG 433
Db 5421 AGTGGGGTTGGG 5433

RESULT 8

US-10-311-455-202/c
; Sequence 202, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311.455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032829.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 202
; LENGTH: 6049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-202

Query Match 33.1%; Score 192.6; DB 12; Length 6049;
Best Local Similarity 66.0%; Pred. No. 4.9e-46;
Matches 279; Conservative 0; Mismatches 144; Indels 0; Gaps 0;
QY 1 ATGGCGACCCAGCGCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db 1049 ATAAGCACCCCAACCTGACCCCAACACAGACTCTAATAACAACTTTTAAATAT 990
QY 61 AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCGACGCCGAC 123
Db 989 AAACCTAAACAAATAAATATATCTATAAACTAACCCGAAACCAACCAACCAAC 930
QY 121 CGCTGACCAAGCATCGGCGCTGCTGGAGACAGTTTGAGACCGTTTCGCGCGGAC 180
Db 929 CGCTACACCAACCATACGACAACTAAATAAATTCGAAAGCCGCTTCGACGAC 870
QY 181 TTCTCTGACCTGGCGCTCAGCTACAGTGCACCGCTCAGCCGACGACGCTTCACC 240
Db 869 TTCTCTAATCTAACGACTCAACTACTATATACCCCAAACTCAACCCCAACAGCTTCACC 810
QY 241 CAGGTTTCCGACGAACTTTTCCAGGGGGCCCTAACTGGGCGCGCTTTGTGGCATCTTT 300
Db 809 CAAATCTCGATAAATTTTTCAAAAAACCACCACTAAACCGCCTTATAACCTTCTTT 750

QY 301 GTCTTTGGGCGTGCCTGTGTCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGTGGGA 360
Db 749 ATCTTTAAAACTACACTATATACTAAAAATATCAACAAAAAATAAAACCACTAATAAAA 690
QY 361 CAAGTCAGGATTGGATGGTGGCCCTACTGGAGACAGCTCTGGCTGACTGGATCCACAGC 420
Db 689 CAAAACAAAAAATAAATAAATTAACCTTACCTTAAACGCAACTAACTAAATCCCAAC 630
QY 421 AGT 423
Db 629 AAT 627

RESULT 9

US-10-029-386-27084
; Sequence 27084, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029.386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27084
; LENGTH: 151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALUE 5.00e-70
; OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11
; OTHER INFORMATION: NT HIT: g114574571, EVALUE 9.00e-80
US-10-029-386-27084

Query Match 25.7%; Score 149.4; DB 12; Length 151;

Best Local Similarity 99.3%; Pred. No. 9.8e-34;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 432 GGCGGAGTTCACAGCTCTATACGGGACCGGGCCCTGGAGGAGGACGCGCTTCGCGGA 491
Db 1 GGCGGAGTTCACAGCTCTATACGGGACCGGGCCCTGGAGGAGGCGCGCTTCGCGGA 60
QY 492 GGGGAACCTGGGATCAGTGAAGACAGTGTGACGGGGCGCTGGCACTGGGGCCCTGGT 551
Db 61 GGGAACCTGGGATCAGTGAAGACAGTGTGACGGGGCGCTGGCACTGGGGCCCTGGT 120
QY 552 AACTGTAGGGGCGCTTTTCTAGCAAGTGA 582
Db 121 AACTGTAGGGGCGCTTTTCTAGCAAGTGA 151

RESULT 10

US-10-029-386-13384
; Sequence 13384, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029.386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288


```

; SOFTWARE: Anco-max Sequence Listing Engine vers. 1.1
; SEQ ID NO 13384
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 2.00e-10
; OTHER INFORMATION: NT HIT: g114751151, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALUE 1.00e-119
US-10-029-386-13384

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Query Match      25.7%   Score 149.4; DB 12; Length 590;
Best Local Similarity 99.3%; Pred. No. 1.2e-33;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 432 GCGGAGTTTCACAGCTCTATACGGGAGCGGGCCCTGGAGGAGCAGCGCCTCTGCGGGA 491
DB 25 GCGGAGTTTCACAGCTCTATACGGGAGCGGGCCCTGGAGGAGCAGCGCCTCTGCGGGA 84
QY 492 GGGGAACCTGGGCATCAGTGAGACAGTCTGACGGGGCCCTGGCACTGGGGCCCTGGT 551
DB 85 GGGGAACCTGGGCATCAGTGAGACAGTCTGACGGGGCCCTGGCACTGGGGCCCTGGT 144
QY 552 AACTGTAGGGCCCTTTTGTAGCAAGTGA 582
DB 145 AACTGTAGGGCCCTTTTGTAGCAAGTGA 175

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RESULT 11
US-09-864-761-17690
; Sequence 17690, Application US/09964761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Cher, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXCN NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aomics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anco-max Sequence Listing Engine vers. 1.1
; SEQ ID NO 17690
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL049829.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
; OTHER INFORMATION: NT HIT: D87461.1, EVALUE 2.00e-79
; OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALUE 8.00e-70
; OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11
US-09-864-761-17690

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```

Query Match      25.5%   Score 148.4; DB 9; Length 150;
Best Local Similarity 99.3%; Pred. No. 1.9e-33;
Matches 149; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 433 GCGGAGTTTCACAGCTCTATACGGGAGCGGGCCCTGGAGGAGCAGCGCCTCTGCGGAG 492
DB 1 GCGGAGTTTCACAGCTCTATACGGGAGCGGGCCCTGGAGGAGCAGCGCCTCTGCGGAG 60
QY 493 GGGAACTGGGCATCAGTGAGGAGCAGTCTGACGGGGCCCTGGCACTGGGGCCCTGGTA 552
DB 61 GGGAACTGGGCATCAGTGAGGAGCAGTCTGACGGGGCCCTGGCACTGGGGCCCTGGTA 120
QY 553 ACTGTAGGGCCCTTTTGTAGCAAGTGA 582
DB 121 ACTGTAGGGCCCTTTTGTAGCAAGTGA 150

```

```

RESULT 12
US-10-169-223-13
; Sequence 13, Application US/10169223
; Publication No. US20030152946A1
; GENERAL INFORMATION:
; APPLICANT: SHIMIZU, Shigeomi
; APPLICANT: TSUJIMOTO, Yoshihide
; TITLE OF INVENTION: BH4-Fused Polypeptides
; FILE REFERENCE: 1422-0537P
; CURRENT APPLICATION NUMBER: US/10/169,223
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: JP 11-371449
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: PCT/JF00/09274
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized DNA for mutant bcl-xL
; FEATURE:
; NAME/KEY: CDS

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/ LOCATION: (1)..(636)
; OTHER INFORMATION:
US-10-169-223-13

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Best Local Similarity 58.3%; Pred. No. 2.4e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

Qy 128 ACCAAGCCATGCGGCGCTGCTGGAGACAGATTGGAGACCCCTTTCCGCGCACCTTCTCTG 187
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RESULT 13
US-09-959-987-9
; Sequence 9, Application US/09959987
; Publication No. US20030040012A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Corporation
; TITLE OF INVENTION: A Detection Method of Protein-Protein Interaction
; FILE REFERENCE: 2001_1695A/WNC/00653
; CURRENT APPLICATION NUMBER: US/09/959,987
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/JP01/01973
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(702)
US-09-959-987-9

Query Match      23.1%; Score 134.6; DB 11; Length 702;
Best Local Similarity 58.3%; Pred. No. 2.4e-29;
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; LOCATION: (1)..(636)
; OTHER INFORMATION:
US-09-925-674a-8.rnpb

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Best Local Similarity 58.3%; Pred. No. 2.5e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

Qy 128 ACCAAGCCATGCGGCGCTGCTGGAGACAGATTGGAGACCCCTTTCCGCGCACCTTCTCTG 187
Db 394 AGCAAGCGCTGAGGAGCGCAGCGCAGCTTTGAATCGCGTACCGGGCGCATTCAGTG 453
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Qy 248 CCGACGAACTTTTCAAGGGGGCCCTAACTGGGGCCGCTGTGTGGCATTTCTTGTCTTTG 307
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Qy 308 GGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGCAAGTGC 367
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RESULT 14
US-09-734-846-1
; Sequence 1, Application US/09734846
; Patent No. US20010097025A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0528
; CURRENT APPLICATION NUMBER: US/09/734,846
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/323,743
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(836)
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
US-09-734-846-1
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238055 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estlin.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
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22: em_gss_mam.*
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27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

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ALIGNMENTS

RESULT : AK015644 1949 bp mRNA linear HTC 05-DEC-2002
LOCUS AK015644 Mus musculus adult male testis cDNA, RIKEN full-length enriched
DEFINITION library, clone:493048B08 product:Bcl2-like 2, full insert
sequence.

ACCESSION AK015644
VERSION AK015644.1 GI:12854052
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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8 430.6 74.0 697 12 BF705666
9 429.8 73.8 854 11 AK013244
10 417 71.6 792 10 BG298789
11 415.4 71.4 623 14 CB578463
12 411.6 70.7 540 9 AW258810
13 391.8 67.3 626 14 CA391923
14 368.8 63.0 643 12 BF1910270
15 358.4 61.6 440 14 CB749817
16 353.2 60.7 559 14 BY704881
17 351.2 60.3 437 14 CB790932
18 335.6 57.7 869 13 BU557268
19 335.6 57.7 872 13 BU557410
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26 294.4 50.6 1053 13 BU931540
27 286.8 49.3 758 12 BF764428
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29 273.4 47.0 430 14 CB760687
30 270 46.4 425 13 BY251598
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33 262.2 45.1 305 13 BY356183
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35 253.4 43.5 353 13 BY312773
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37 246.4 42.3 375 13 BY302913
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REFERENCE
AUTHORS

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kuni, H., Akiyama, J., Nishi, K., Kitesuna, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, N., Yoneda, Y., Ishikawa, T., Osawa, K., Tanaka, T., Matsura, S., Kawai, C., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

TITLE

JOURNAL
MEDLINE
PUBMED

20530913
11076861

REFERENCE
AUTHORS

4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R., Kado, K., Matsuda, H., Ashburner, M., Bata, C. V. S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kouchiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaudo, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staab, J. F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Saka, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, J., Bojunga, N., Carninci, P., de Bona, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gai, D. A., Kamiya, M., Lee, N. H., Lyons, P., McWhinnery, L., Mashima, J., Mazzarelli, N., Mombauts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seva, T., Shibata, Y., Sorch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S. and Hayashizaki, Y.

TITLE

JOURNAL
MEDLINE
PUBMED

21085660
11217851

REFERENCE
AUTHORS

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

TITLE

JOURNAL
AUTHORS

6 (bases 1 to 1949)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, P., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

TITLE

JOURNAL

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase

COMMENT

and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATCTCGATTAAATTAATCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size compressed longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC 1. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

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source

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BASE COUNT 396 a 473 c 628 g 452 t
ORIGIN

Query Match 99.5%; Score 578.8; DB 11; Length 1949;
Best Local Similarity 99.7%; Pred. No. 2.4e-135;
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DB 492 CAAGTGCAGGATTGGATGGTGGCTTACCTGGAGACAGCTCTGGCTGACTGGATCCAC 551
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BY715200									
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DEFINITION	BY715200	CDNA clone 4930488D08 5', mRNA sequence.							
ACCESSION	BY715200	EST.							
VERSION	BY715200.1	GI:27128317							
KEYWORDS									
SOURCE	Mus musculus	(house mouse)							
ORGANISM	Mus musculus								
REFERENCE									
AUTHORS									

R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Katanabe, Y., Wells, C., Wilming, L.G., Wynehaw-Boris, A., Yanagisawa, Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, C., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, M., Imotani, K., Ishii, Y., Itoh, M., Kadowa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physiological and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.go.jp

URL: http://genome.gsc.riken.go.jp/

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, M., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kadowa, I., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken. Prepared mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

Location/Qualifiers

1..969

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/mol_type="mRNA"

/strain="C57BL/6J"

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/dev_stage="adult"

/lab_host="GOLR"

/clone_lib="RIKEN full-length enriched, adult male testis"

/note="Site 1: XhoI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'

FEATURES

source


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KEYWORDS SOURCE ORGANISM
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 804)
AUTHORS Ansong, W., Wirkner, J., Mewes, K., Weil, B. and Wiemann, S.
TITLE EST (Ansong, W., Wirkner, J., Mewes, K., Weil, B. and Wiemann, S.)
JOURNAL Unpublished
COMMENT Contact: Ansong W
MIPS Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No 5' sequence available.
This clone (DKFZp761D0816) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clones@rzpd.de.
FEATURES
Location/Qualifiers
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Matches 541; Conservative 0; Mismatches 39; Indels 2; Gaps 2;
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QY 301 GTCTTTGGGGCTGCCCTGTGTGCTTGAGAGTGTCAACAAGAAATGGAGCCCTTTGTGGGA 360
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DB 494 CAAGTGAGGAGATTGGATGGTGGCTTACTTGAGACACGCTTGGCTGACTGGATCCACAGC 553
QY 421 AGTGGCGGCTGGCGGAGTTTCACAGCTCTATACGGGACGGGCGCTTGGAGGAGGACGG 480
DB 554 AGTGGGCGCTGGCGGAGTTTCACAGCTCTATACGGGAC - GGGCGCTTGGAGGAGGCGG 612
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Db 613 CGTCTGGGAGGGAACTGGGCATCAGTAGGACAGTGCTGACGGGGCGCTGGCACC 671
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mRNA sequence.
ACCESSION BE793530
VERSION BE793530.1 GI:10214832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1030)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCRD/DRP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Place: BLCM800 row: P column: 04
High quality sequence start: 5
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insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Best Local Similarity 90.7%; Pred. No. 1.9e-114;
Matches 528; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
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QY 61 AGGCTGAGGAGAGGGTTATGCTGTGGAGCTGCGCTGGGAGAGCCAGCCCGAC 120
DB 204 AAGCTGAGGAGAGGGTTATGCTGTGGAGCTGCGCTGGGAGAGCCAGCAGCTGAC 263
QY 121 CCGCTGCACCAAGCCATCGGCGCTCTCGAGACGAGTTTGAGACCCGTTCCGCCGACC 180
DB 264 CCACCTGCACCAAGCCATCGGCGCAGCTGGAGATGAGTTTCGAGACCCGCTTCGGCGCACC 323
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Db      564 AGTGGGGGCTGGCGGAGTTTACAGCTCTATACGGGGACGGGCGCTTGGAGAGGACAGG 623
QY      481 CGTCTGGGGAGGGAACTGGGCATCAGTGGAGACAGTCTGACGGGGGCGTGGCACTG 540
Db      624 CGTCTGGGGAGGGAACTGGGCATCAGTGGAGACAGTCTGACGGGGGCGTGGCACTG 683
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ACCESSION  BF785386
VERSION     1
KEYWORDS    S., mRNA sequence.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC);
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-r@mail.nih.gov
          Tissue Procurement: Jeffrey E. Green, M.D.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
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              Average insert size 1.75 kb. Constructed by Life
              Technologies. Note: this is a NCI_CGAP Library. |"
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BASE COUNT 166 a 212 c 296 g 141 t
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Matches 530; Conservative 0; Mismatches 10; Indels 9; Gaps 7;

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QY      81 TGCTGTGAGAGTGGCCCTGGGGAGGCGCAGCGCCGACCCGCTGCAACAGCCATGG 140
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QY      141 GGCTGTGTGAGAGAGAGTGTGAGACCGCTTTCCGCCGACCTTCTCTGACCTGCCGCTCA 200
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QY      201 GCTACACGTGACCCCGAGGCTCAGCCAGCAAGCGCTTCAACCAGGTTTCCGACGAACTTT 260
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Db      240 CAAAGGGGGCGCTTAACCTGGGGCGCTGTTGGGCAATCT--TGCTTTGGGGCTGCCCTGTG 296
QY      321 TGCTGAGAGTGTCAACAAGAAATGAGCGCTTTGGTGGGACAGTGCAGGATTTGGATGGT 380
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QY      381 GGCTTACCTGGAGACACGCTTGGCTGACTGGATCCACAGCAGTGGCGGCTGGCGGAGATT 440
Db      356 GGCTTACCTGGAGACACGCTTGGCTGACTGGATCCACAGCAGTGGCGGCTGGCGGAGATT 415
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QY      501 GGCATCAGTGAGGACAGTGTGACGGGGCGCGTGGCACTGGGGGGCGCTTGAATCTTAGG 560
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QY      561 GGCCTTTT 569
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ACCESSION  BI770566
VERSION     BI770566.1 GI:5762144
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 697)
          NIH-MGC http://mgc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished
          Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-r@mail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM1526 row: k column: 15
          High quality sequence start: 21
          High quality sequence stop: 695.
          Location/Qualifiers

FEATURES

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/lab_host="DH10B"
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anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is cDNA
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 036. Note:
this is a NIH_MGC Library."
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ORIGIN

Query Match      74.0%; Score 430.6; DS 12; Length 697;
Best Local Similarity 92.0%; Pred. No. 4.4e-98;
Matches 509; Conservative 0; Mismatches 39; Indels 5; Gaps 5;

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QY 61 AGCGTGAGCGAAGAGGTTATCTCTGTGAGCTGGCCCTGGGGAAGGCCACGCGCCGAC 120
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QY 205 AAGCTGAGCGACAGAGGTTATCTCTGTGAGCTGGCCCGGGAGGGCCGACGAGCTGAC 264
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RESULT 9
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LOCUS
DEFINITION
AK013244
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sequence.
AK013244
ACCESSION
AK013244.1 GI:12850487

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KEYWORDS

SOURCE
Xus musculus (house mouse)
Xus musculus

ORGANISM
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PubMed
10349636

REFERENCE

AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
2049374
PubMed
11042159

REFERENCE

AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Tonega, Y., Ishikawa, T., Ozawa, K., Tanaka, I., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE
20530913
PubMed
11076861

REFERENCE

AUTHORS
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, T.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Bataiov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G.,
Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,
Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.,
and Hayashizaki, Y.

REFERENCE

AUTHORS
The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase 1 & 11 Team.
TITLE
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL
Nature 420, 563-573 (2002)
MEDLINE
21085660
PubMed
11217851

REFERENCE

AUTHORS
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,

Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5', CAGAGAGAGAGATCAAGAGCTTTT'TTTT'TT'TVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter of sequence [5', CAGAGAGATTCGAGTTTAATTAATATCCCGCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
 Host: SOLR.

FEATURES

source
 Location/Qualifiers
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 /db_xref="MGI:1902183"
 /db_xref="taxon:10090"
 /clone="2810435A13"
 /tissue_type="whole body"
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 /dev_stage="10, 11 days embryo"
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 178 a 229 c 264 g 183 t

CDS

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 178 a 229 c 264 g 183 t

BASE COUNT

178 a 229 c 264 g 183 t
 Query Match 73.8%; Score 429.8; DB 11; Length 854;
 Best Local Similarity 99.5%; Pred. No. 7.3e-98;
 Matches 431; Conservative 0; Mismatches 2; Indels 0; Gaps 3;

QY 1 ATGGCACCACCCAGCTCAACCCAGACACACGGGCTCTAGTGGCTGACCTTTAGGCTAT 60
 DB 196 ATGGCACCACCCAGCTCAACCCAGACACACGGGCTCTAGTGGCTGACCTTTAGGCTAT 255
 QY 61 AGGCTGAGGAGAGAGGTTATGTCTGTGAGCTGGCCCTGGGAGGCCAGCCGCGGAC 120
 DB 256 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTGGCCCTGGGAGGCCAGCCGCGGAC 315
 QY 121 CCCTGCACCAAGCCATGCGGGCTGTGGAGAGAGAGTTTGAGACCCGTTTCCGCGGAC 180
 DB 316 CCCTGCACCAAGCCATGCGGGCTGTGGAGAGAGAGTTTGAGACCCGTTTCCGCGGAC 375
 QY 181 TTCTCTGACCTGCGCGCTAGCTACAGTGAACCCAGGCTCAGCCAGCAAGCGTTTACC 240
 DB 376 TTCTCTGACCTGCGCGCTAGCTACAGTGAACCCAGGCTCAGCCAGCAAGCGTTTACC 435

QY 241 CAGGTTTCCGACGAACCTTTTCCAAAGGGGSCCTTAACCTGGGGCGTCTTGTGSCATTTCTT 300
 DB 436 CAGGTTTCCGACGAACCTTTTCCAAAGGGGSCCTTAACCTGGGGCGTCTTGTGSCATTTCTT 495
 QY 301 GTCTTTGGGGCTCCCTGTGTCTGAGAGTGTCACAAAGAAATGGAGCTTTGGTGGGA 360
 DB 496 GTCTTTGGGGCTCCCTGTGTCTGAGAGTGTCACAAAGAAATGGAGCTTTGGTGGGA 555
 QY 361 CAAGTGCAGGATTGGATGGTGGCTACCTACCTGGAGACACGCTCTGGCTGACTGGATCCACAGC 420
 DB 556 CAAGTGCAGGATTGGATGGTGGCTACCTACCTGGAGACACGCTCTGGCTGACTGGATCCACAGC 615
 QY 421 AGTGGCGGCTGGG 433
 DB 616 AGTGGCGGCTGGG 628

RESULT 10

BG298789 792 bp mRNA linear EST 21-FEB-2003
 DEFINITION 602396527F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4511215 5', mRNA sequence.

ACCESSION

BG298789.1 GI:13063794

VERSION

BG298789

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 792)

AUTHORS

NIH-MGC http://mgi.nci.nih.gov/

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cga@b6-mail.nih.gov

Tissue Procurement

The Cepko Laboratory

cDNA Library Preparation

Life Technologies, Inc.

cDNA Library Arrayed by

The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by

Incyte Genomics, Inc.

Clone distribution

MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10394 row: e column: 08

High quality sequence stop: 723.

Location/Qualifiers

1..792

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:4511215"

/tissue_type="retina"

/lab_host="DHI08 (phage-resistant)"

/clone_lib="NIH_MGC_94"

/notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

174 a 201 c 246 g 171 t

BASE COUNT

174 a 201 c 246 g 171 t

ORIGIN

Query Match 71.6%; Score 417; DB 10; Length 792;
 Best Local Similarity 98.8%; Pred. No. 1.2e-94;
 Matches 431; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 ATGGGACCCAGCTCAACCCAGACACACGGGCTCTAGTGGCTGACCTTTAGGCTAT 60
 DB 99 ATGGGACCCAGCTCAACCCAGACACACGGGCTCTAGTGGCTGACCTTTAGGCTAT 158
 QY 61 AGGCTGAGGAGAGGTTATGTCTGTGAGCTGGCCCTGGGAGGCCAGCCGCGGAC 120
 DB 159 AAGCTGAGGAGAGGTTATGTCTGTGAGCTGGCCCTGGGAGGCCAGCCGCGGAC 218

vector (5' site CACTGTGTG, 3' site CACCATCTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGCTCTAAAGGTGG and 3' end primer CGACCTGCAGCTCGAGACA."

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BASE COUNT 98 a 165 c 170 g 137 t
ORIGIN
Query Match 70.7%; Score 411.6; DB 9; Length 540;
Best Local Similarity 98.8%; Pred. No. 2.5e-93;
Matches 425; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1 ATGGGACCCAGCCTCAACCCAGACACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
DB 112 ATGGGACCCAGCCTCAACCCAGACACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 171
QY 61 AGGCTGAGGACAGAGGTTATCTGTGGAGCTGGCCCTGGGAGAGGCCAGCCGCGAC 120
DB 172 AAGCTGAGGACAGAGGTTATCTGTGGAGCTGGCCCTGGGAGAGGCCAGCCGCGAC 231
QY 121 CGGCTGCACCAAGCCATGCGGCTGTGTGAGACGAGTTTGAGACCCGTTTCGCGCGAC 180
DB 232 CGGCTGCACCAAGCCATGCGGCTGTGTGAGACGAGTTTGAGACCCGTTTCGCGCGAC 291
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DB 292 TTCTGTGACTGGCGCTCAGCTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 351
QY 241 CAGGTTTCGAGCAACTTTTCCAAAGGGGCCCTAACTGGGGCGCTCTGTGGCATCTTT 300
DB 352 CAGGTTTCGAGCAACTTTTCCAAAGGGGCCCTAACTGGGGCGCTCTGTGGCATCTTT 411
QY 301 GTCTTTGGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
DB 412 GTCTTTGGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 471
QY 361 CAAGTGCAGGATGGATGTGGCTTACCTGAGACACAGTCTGGCTGATCGATGCACAGC 420
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QY 421 AGTGGCGCT 430
DB 531 AGTGGCGCT 540

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RESULT 13
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LOCUS
DEFINITION
cs20c09.y1 Human Retinal pigment epithelium/choroid cDNA
5', mRNA sequence.
UN-normalized, unamplified; cs Homo sapiens cDNA clone cs20c09
CA391923
VERSION
CA391923.1 GI:24724221
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 626)
Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Beha,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human RPE/choroid for the
NEI Bank Project: Over 6000 non-redundant transcripts, novel genes
and splice variants
Mol. Vis. 8 (4), 205-220 (2002)
JOURNAL
MEDLINE
22103460
PUBMED
12107410
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA

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Tel: 301 402 3452
Fax: 301 496 0078
E-mail: graeme@helix.nih.gov
Plate: 20 row: c column: 09
Seq primer: M13p1 reverse primer (ABI).
FEATURES
Location/Qualifiers
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/dev_stage="Adult"
/lab_host="EMDH10B"
(clone lib="Human Retinal pigment epithelium/choroid cDNA
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/notes="Organ: Eye; Vector: pCMVSPORT6; Two different donor
eyes (75-80 years old) yielded approximately 600 mg of
dissected RPE/choroid tissue. This in turn yielded 340 ug
of total RNA and 7 ug of mRNA. A directionally cloned cDNA
library in the pCMVSPORT6 vector was constructed at Life
Technologies (Rockville, MD; now part of Invitrogen Corp),
essentially following the protocols of the SuperScript
Plasmid System (Invitrogen Corp.
<http://www.invitrogen.com/>). The library code
designation was cs. For this library, cDNA inserts were
cloned into the NotI/MluI sites of the vector. EST
analysis was performed on the unamplified library at the
NIH Intramural Sequencing Center (NISC)."
BASE COUNT 108 a 202 c 197 g 118 t 1 others
ORIGIN
Query Match 67.3%; Score 391.8; DB 14; Length 626;
Best Local Similarity 91.6%; Pred. No. 2.6e-88;
Matches 414; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 1 ATGGCGACCCAGCCTCAACCCAGACACACAGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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QY 61 AGGCTGAGGACAGAGGTTATGTCTGTGGAGCTGGCCCTGGGAGAGGCCAGCCGCGAC 120
DB 235 AGGCTGAGGACAGAGGTTATGTCTGTGGAGCTGGCCCGGAGGCCAGCAGCTGAC 294
QY 121 CGGCTGCACCAAGCCATGCGGCTGTGTGAGACGAGTTTGAGACCCGTTTCGCGCGAC 180
DB 295 CGGCTGCACCAAGCCATGCGGCGAGCTGGAGATGAGTTTCGAGACCCGCTTCGCGCGAC 354
QY 181 TTCTGTGACTGGCGCTCAGCTACAGTGACCCAGGCTCAGCCAGCAAGCCTTCACC 240
DB 355 TTCTGTGATCTGGCGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACACGCTTCACC 414
QY 241 CAGGTTTCGAGCAACTTTTCCAAAGGGGCCCTAACTGGGGCGCTCTGTGGCATCTTT 300
DB 415 CAGGTTTCGAGCAACTTTTCCAAAGGGGCCCTAACTGGGGCGCTCTGTAGCCTTTCTT 474
QY 301 GTCTTTGGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGGAGCCTTTGTGGGA 360
DB 475 GTCTTTGGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAGATGGAACCACTGGTGGGA 534
QY 361 CAAGTGCAGGATGGATGGTGGCTACCTGGAGACAGCTGTGCTGACTGACTGCATCCACAGC 420
DB 535 CAAGTGCAGGATGGATGGTGGCTACCTGGAGACGCGGCTGGCTGACTGACTGCATCCACAGC 594
QY 421 AGTGGCGCTGGGCGAGTTTCACAGCTCTATA 452
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RESULT 14
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BI910270 BI910270 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218294 5',

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mRNA sequence.
 Bi910270
 VERSION Bi910270.1 GI:16173653
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 643)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LMAX1548 row: j column: 23
 High quality sequence step: 643.
 Location/Qualifiers
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 /clone_lib="NIH-MGC-1.8"
 /note="Vector: pCMV-SPC16; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library."
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 Matches 415; Conservative 0; Mismatches 62; Indels 1; Gaps 1;
 QY 1 ATGGGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTCTAGGCTAT 60
 Db 140 ATGGGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAGACTTTGTAGGTTAT 199
 QY 61 AGGCTGAGGACAGAGGTTATGTCTGTGAGCTGGCCCTGGGGAAGGCCAGCCGCCGAC 120
 Db 200 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGGCCCGGGGAGGCCAGCAGCTGAC 259
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 Db 260 CGCTGCACCAACCCATGGGGCAGCTGTGAGATGAGTTTCGAGACCCGCTTCGCGGCC 319
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 Db 320 TTCTGTAGCTGGGGCTCAGCTGATGTGACCCAGGCTCAGCCCAACAGCCTTACCC 379
 QY 241 CAGGTTTCGACGAATTTTCAAGGGGCGCTTAACCTGGGGCGCTTGTGGCATTTT 300
 Db 380 CAGGTTCCGATGAATTTTCAAGGGGCGCCCACTGGGGCGCTTGTAGCTTCTT 439
 QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGA-AATGGAGCCTTTGGTGG 359
 Db 440 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAAGGAGCATGGAACCACTGTGG 499
 QY 360 ACAAAGTCAGGATTGGATGGTGGCTACCTCGAGACACGCTCTGGCTGACTGATCCACAG 419

Db 500 ACAAAGTCAGGATTGGATGGTGGCTTACCTGGAGACGGCTGGCTGACTGGATCCACAG 559
 QY 420 CAGTGGCGGCTGGCGGAGTTTCACAGCTCTATACGGGAGCGGCGCTGGAGGAGCA 477
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 1 to 440)
 AUTHORS Angen EST Program.
 TITLE Angen Rat EST Program
 JOURNAL Unpublished
 COMMENT Contact: Dan Fitzpatrick
 Angen, Inc
 One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
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 Location/Qualifiers
 1..440
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 Matches 368; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 QY 65 TGAGGCGAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCGAGCCGAC 124
 Db 50 TGAGGCGAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCGAGCCGAC 109
 QY 125 TGCACCAAGCCATCGGGCTGTGTGAGACGAGTTTGAGACCCGTTTCCGGCGCACCTTCT 184
 Db 110 TGCACCAAGCCATCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCGGGCGCACCTTCT 169
 QY 185 CTGACCTGGCGCTCAGCTACAGTACCCAGCTCAGCCAGCCAGCAAGCTTACCCAGG 244
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 QY 305 TTGGGGCTGGCCCTGTGTGTGTGAGAGTGTCAACAAAGAAAATGGAGCCCTTTCGTGGGACA 364
 Db 290 TTGGGGCTGGCCCTGTGTGTGTGANAGTGTCAACAAAGAAAATGGAGCCATTTGGTGGACA 349
 QY 365 TGCAGGATTGGATGGTGGCTTACCTGAGACACGCTCTGGCTGACTGATCCACAGCAAGT 424
 Db 350 TGCAGGATTGGATGGTGGCTTACCTGAGACACGCTTGGCTGACTGATCCACAGCAAGT 409
 QY 425 CGGGCTGGGGGAGTTTCACAGCTCTATACG 455
 Db 410 GGGGCTGGGGGAGTTTCACAGCTCTATACG 440

Search completed: October 27, 2003, 13:50:45
Job time : 1468.74 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 24, 2003, 10:27:45 ; Search time 60 Seconds
(without alignments)
510.570 Million cell updates/sec

Title: US-09-925-674A-9
Perfect score: 1009
Sequence: 1 MATPASTPTDTRALVADPVG.....LTGAVAGALVTVGAFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1006	99.7	193	AAV05531	Mouse Bcl-w protei
2	1002	99.3	193	AAW61391	Rat bcl-y protei
3	1002	99.3	193	AAW97391	The rat bcl-y pro
4	997	98.8	192	AAW97393	Protein sequence o
5	997	98.8	192	AAW05530	Human Bcl-w protei
6	992	98.3	193	AAW61392	Human bcl-y protei
7	992	98.3	193	AAW97392	The human bcl-y pr
8	990	98.1	193	AAW36047	Human bcl-w protei
9	990	98.1	193	AAV05532	Human Bcl-w protei

10	987	97.8	192	20	AAW97394	Mammalian bcl-y pr
11	970.5	96.2	192	20	AAV05533	Mouse Bcl-w protei
12	879	87.1	168	18	AAW36048	Mouse Bcl-w protei
13	811.5	80.4	190	23	AAO18223	Human Bcl-Rambo BH
14	756	74.9	365	19	AAW59884	Amino acid sequenc
15	756	74.9	365	23	ABG95556	Human novel secret
16	429.5	42.6	411	22	AAU00219	Bcl-XL-DTR apoptos
17	427.5	42.4	237	23	ABG78480	Wild type BclXl pr
18	425.5	42.2	233	22	AAW73303	Rat wild-type Bcl-
19	424.5	42.1	233	16	AAW68887	Human thymus BCL-X
20	424.5	42.1	233	17	AAW05821	Bcl-XL protein. H
21	424.5	42.1	233	18	AAW31530	Human anti-apoptot
22	424.5	42.1	233	21	AAW83223	Bcl-x polypeptide.
23	424.5	42.1	233	21	AAW69969	Human Bcl-XL prote
24	424.5	42.1	233	22	AAW64262	Human Bcl-XL prote
25	424.5	42.1	233	22	AAW50538	Human Bcl-XL prote
26	424.5	42.1	233	22	AAW47515	Protein encoded by
27	422	41.8	225	18	AAW19396	"Deprenyl" (RTM)-i
28	421.5	41.8	233	22	AAW73304	Mutant rat Bcl-XL
29	412.5	40.9	239	22	AAW64037	Human Bcl-2 protei
30	411.5	40.8	152	24	AAW97960	Bcl-XL. Homo sapi
31	409	40.5	236	22	AAW35131	Murine Bcl-2. Mus
32	409	40.5	236	23	AAW76554	A human Bcl-2 polyp
33	408.5	40.5	239	20	AAW87810	Murine Bcl-2 prot
34	408.5	40.5	239	22	AAW74127	Human Bcl-2. Homo
35	408.5	40.5	239	22	AAW35130	Human Bcl-2. Homo
36	408.5	40.5	239	23	ABG78478	Human Bcl2 mutant
37	408.5	40.5	239	23	ABG78479	Human Bcl2 mutant
38	408.5	40.5	239	23	AAW76553	Human Bcl-2 polype
39	408.5	40.5	272	24	ABR41675	Human DTHP cell
40	406.5	40.3	239	9	AAW80987	Sequence of bcl-2-
41	406.5	40.3	239	14	AAW42312	Bcl-2 oncogene pro
42	406.5	40.3	239	16	AAW70331	Human bcl-2 protei
43	406.5	40.3	239	16	AAW71404	Human bcl-2 alpha
44	406.5	40.3	239	19	AAW40217	Human bcl-2. Homo
45	406.5	40.3	239	20	AAW87812	A human Bcl-2-alph

AL-GNMENTS

RESULT 1
ID AAY05531 standard; Protein; 193 AA.
XX
XX AAY05531;
AC
XX
DT 05-JUL-1999 (first entry)
DE Mouse Bcl-w protein essential for spermatogenesis.
XX
XX Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW animal model.
XX
XX Mus sp.
XX
XX W09513710-Ai.
XX
XX 25-MAR-1999.
XX
XX 16-SEP-1998; 98WO-AU00764.
XX
XX 16-SEP-1997; 97AU-0009228.
XX
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
XX Adams J, Cory S, Gibson L, Koentgen P, Print C;
XX WPI; 1999-243890/20.
XX N-PSDB; AAX25133.
XX
XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX protein associated with Bcl-w

XX	Claim 2; Page 35; 52pp; English.
PS	The present sequence is mouse bcl-w, a pro-survival member of the
XX	bcl-2 family which is widely expressed and which is essential for
CC	spermatogenesis. The invention relates generally to a method of
CC	treatment and to an animal model for the identification of
CC	molecules and genetic sequences useful for inducing or reducing
CC	fertility of male animals. Methods are provided for the treatment
CC	of infertility, or for reducing fertility, by modulating
CC	spermatogenesis. An animal model carries a mutation is at least
CC	one allele of the human or murine bcl-w gene (see AAM25132-35) or in
CC	a gene associated with bcl-w. Such animals have disorganised
CC	seminiferous tubules and are substantially infertile, but possess no
CC	other major abnormalities as determined by histological examination.
CC	They can be used to screen for therapeutic molecules including
CC	genetic sequences capable of inducing, enhancing or otherwise
CC	facilitating spermatogenesis in animals, or which can induce
CC	infertility.
XX	
SQ	Sequence 193 AA;
	Query Match: 99.7%; Score 1006; DB 20; Length 193;
	Best Local Similarity 99.5%; Pred. No. 7e-102;
	Matches 192; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY	1 MATPASTPTETRALVADFGVYLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
DB	1 MATPASTPTETRALVADFGVYLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
QY	61 FSDLAALQLHVTGSAQQORFTQVSDELFOGGPNWGRLVAFVFVGAALCAESVNKEMEPLVG 120
DB	61 FSDLAALQLHVTGSAQQORFTQVSDELFOGGPNWGRLVAFVFVGAALCAESVNKEMEPLVG 120
QY	121 QVQDMNVAYLETRLDWIHSSGGWAEEFTALYDGLAEARLRREGNWSVRTVLITGAVAL 180
DB	121 QVQDMNVAYLETRLDWIHSSGGWAEEFTALYDGLAEARLRREGNWSVRTVLITGAVAL 180
QY	181 GALVTVGAFFAASK 193
DB	181 GALVTVGAFFAASK 193
RESULT 2	
AAM6139:	
ID	AAW61391 standard; Protein; 193 AA.
XX	
AC	AAW61391;
DT	02-OCT-1998 (first entry)
DE	Rat bcl-y protein.
XX	bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
OS	Rattus sp.
XX	US5789201-A.
PD	04-AUG-1998.
PF	11-FEB-1997; 97US-0798897.
PR	23-FEB-1996; 96US-0012201.
PR	11-FEB-1997; 97US-0798897.
PA	(COCE-) COCENSYS INC.
PI	Guastella J;
XX	WPI; 1998-446079/38.
DR	N-PSDB; AAV28333.
XX	

PT	Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT	producing recombinant protein for use in treating uncontrolled cell
XX	growth e.g. cancers
XX	Example; Fig 3A; 27pp; English.
XX	The mammalian bcl-y protein is a member of the bcl-2 family, components
CC	in the cell death pathway. The bcl-2 family have both apoptotic activity
CC	and the apoptosis blocking activity. bcl-y falls in the apoptosis
CC	activity category. The recombinant protein may be used to prevent
CC	uncontrolled cell growth, either by its direct administration to
CC	recombinant genetic constructs to increase its expression in vivo. Also,
CC	antisense constructs can be used in disorders where prevention of cell
CC	death is desired.
XX	
SQ	Sequence 193 AA;
	Query Match: 99.3%; Score 1002; DB 19; Length 193;
	Best Local Similarity 99.0%; Pred. No. 1.9e-101;
	Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	1 MATPASTPTETRALVADFGVYLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
DB	1 MATPASTPTETRALVADFGVYLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
QY	61 FSDLAALQLHVTGSAQQORFTQVSDELFOGGPNWGRLVAFVFVGAALCAESVNKEMEPLVG 120
DB	61 FSDLAALQLHVTGSAQQORFTQVSDELFOGGPNWGRLVAFVFVGAALCAESVNKEMEPLVG 120
QY	121 QVQDMNVAYLETRLDWIHSSGGWAEEFTALYDGLAEARLRREGNWSVRTVLITGAVAL 180
DB	121 QVQDMNVAYLETRLDWIHSSGGWAEEFTALYDGLAEARLRREGNWSVRTVLITGAVAL 180
QY	181 GALVTVGAFFAASK 193
DB	181 GALVTVGAFFAASK 193
RESULT 3	
AAM97391:	
ID	AAW97391 standard; Protein; 193 AA.
XX	
AC	AAW97391;
DT	20-MAY-1999 (first entry)
XX	The rat bcl-y protein.
XX	Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KM	programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KM	head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KM	multiple sclerosis; myocardial infarction; vitally induced cell death;
KM	aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KM	premature cell death; cell death stimulator; prolonged cell life span;
KM	Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KM	parasite.
XX	Rattus sp.
OS	US5883229-A.
XX	16-MAR-1999.
PD	25-NOV-1997; 97US-0978523.
PF	23-FEB-1996; 96US-0012201.
PR	11-FEB-1997; 97US-0798897.
PR	25-NOV-1997; 97US-0978523.
XX	(COCE-) COCENSYS INC.
PA	Guastella J;
XX	


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XX OS Homo sapiens.
XX PN MO9913710-A1.
XX PD 25-MAR-1999.
XX PF 16-SEP-1998; 98MO-AU00764.
XX PR 16-SEP-1997; 97AJ-0009228.
XX PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX PI Adams J, Cory S, Gibson L, Koenigen F, Print C;
XX WPI; 1999-243890/20.
XX DR N-PSDB; AAX25132.
XX PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX PT protein associated with Bcl-w
XX PS Claim 2; Page 33; 52pp; English.
XX The present sequence is human Bcl-w, a pro-survival member of the
XX Bcl-2 family which is widely expressed and which is essential for
XX spermatogenesis. The invention relates generally to a method of
XX treatment and to an animal model for the identification of
XX molecules and genetic sequences useful for inducing or reducing
XX fertility of male animals. Methods are provided for the treatment
XX of infertility, or for reducing fertility, by modulating
XX spermatogenesis. An animal model carries a mutation is at least
XX one allele of the human or murine bcl-w gene (see AAX25132-35) or in
XX a gene associated with bcl-w. Such animals have disorganised
XX seminiferous tubules and are substantially infertile, but possess no
XX other major abnormalities as determined by histological examination.
XX They can be used to screen for therapeutic molecules including
XX genetic sequences capable of inducing, enhancing or otherwise
XX facilitating spermatogenesis in animals, or which can induce
XX infertility.
XX SQ Sequence 193 AA;
Query Match 98.8%; Score 997; DB 20; Length 193;
Best Local Similarity 98.4%; Pred. No. 6.8e-10; Indels 0; Gaps 0;
Matches 190; Conservative 2; Mismatches 1;
QY 1 MATPASTPTDTRALVADFGVYLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
Db 1 MATPASAPDTRALVADFGVYLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAALQHLVTPGSAQQRFTQVSDDELFGGPNWGRLVAFVFGAALCAESVKNEMEPLVG 120
Db 1 MATPASAPDTRALVADFGVYLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAALQHLVTPGSAQQRFTQVSDDELFGGPNWGRLVAFVFGAALCAESVKNEMEPLVG 120
Db 61 FSDLAALQHLVTPGSAQQRFTQVSDDELFGGPNWGRLVAFVFGAALCAESVKNEMEPLVG 120
QY 121 QVQDMWVAYLETRLDWTHSSGGWAEFTALYDGDGALEEARLRREGNWSVRTVLTGVAL 180
Db 121 QVQDMWVAYLETRLDWTHSSGGWAEFTALYDGDGALEEARLRREGNWSVRTVLTGVAL 180
QY 181 GALVTVGAFASK 193
Db 181 GALVTVGAFASK 193
RESULT 6
AAW61392
ID AAW61392 standard; Protein; 193 AA.
XX AC AAW61392;
XX 02-OCT-1998 (first entry)
XX Human bcl-y protein.
XX
bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
KW Homo sapiens.
OS US5789201-A.
PN 04-AUG-1998.
PD 11-FEB-1997; 97US-0798897.
PF 23-FEB-1996; 96US-0012201.
PR 11-FEB-1997; 97US-0798897.
XX (COCE-) COCENSYS INC.
XX Guastella J;
XX WPI; 1998-446079/38.
XX DR N-PSDB; AAV28334.
XX PT Nucleic acids encoding B-cell lymphoma-y protein - useful for
XX PT producing recombinant protein for use in treating uncontrolled cell
XX PT growth e.g. cancers
XX Example; Column 17/18; 27pp; English.
XX The mammalian bcl-y protein is a member of the bcl-2 family, components
XX in the cell death pathway. The bcl-2 family have both apoptotic activity
XX and the apoptosis blocking activity. bcl-y falls in the apoptosis
XX activity category. The recombinant protein may be used to prevent
XX uncontrolled cell growth, either by its direct administration to
XX recombinant genetic constructs to increase its expression in vivo. Also,
XX antisense constructs can be used in disorders where prevention of cell
XX death is desired.
XX SQ Sequence 193 AA;
Query Match 98.3%; Score 992; DB 19; Length 193;
Best Local Similarity 97.9%; Pred. No. 2.4e-100; Indels 0; Gaps 0;
Matches 189; Conservative 2; Mismatches 2;
QY 1 MATPASTPTDTRALVADFGVYLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
Db 1 MATPASAPDTRALVADFGVYLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAALQHLVTPGSAQQRFTQVSDDELFGGPNWGRLVAFVFGAALCAESVKNEMEPLVG 120
Db 61 FSDLAALQHLVTPGSAQQRFTQVSDDELFGGPNWGRLVAFVFGAALCAESVKNEMEPLVG 120
QY 121 QVQDMWVAYLETRLDWTHSSGGWAEFTALYDGDGALEEARLRREGNWSVRTVLTGVAL 180
Db 121 QVQDMWVAYLETRLDWTHSSGGWAEFTALYDGDGALEEARLRREGNWSVRTVLTGVAL 180
QY 181 GALVTVGAFASK 193
Db 181 GALVTVGAFASK 193
RESULT 7
AAW97392
ID AAW97392 standard; Protein; 193 AA.
XX AC AAW97392;
XX 20-MAY-1999 (first entry)
XX The human bcl-y protein.
XX
Rat bcl-y protein; Bcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;

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KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
 KW parasite.
 XX
 OS Homo sapiens.
 XX
 PN US5883229-A.
 XX
 XX 16-MAR-1999.
 PD
 XX
 XX 25-NOV-1997; 97US-0978523.
 PF
 XX
 XX 23-FEB-1996; 96US-012201.
 PR
 XX 11-FEB-1997; 97US-0798897.
 PR
 XX 25-NOV-1997; 97US-0978523.
 XX
 XX (COCE-) COCENSYS INC.
 PA
 XX
 XX Guastella J;
 PI
 XX WPI; 1999-214150/18.
 DR
 DR N-PSDB; AAX15946.
 XX
 XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful
 PT for modulating programmed cell death
 XX
 XX Claim 1: Columns 17-18; 26pp; English.
 PS
 XX The present sequence represents human bcl-y protein (Hbcl-y). The
 CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and
 CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
 CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
 CC proteins may be used to treat conditions associated with a disruption of
 CC the cell death pathway. If they act as cell death inhibitors, they may be
 CC used in therapies to treat subjects suffering from: strokes, head trauma,
 CC Alzheimer's Disease, neural and muscular degenerative diseases
 CC (especially multiple sclerosis), myocardial infarction, vitally induced
 CC cell death, aging, spinal cord injuries and ankyrotic lateral
 CC sclerosis- conditions where cells under go premature cell death as a
 CC result of triggers which may or may not be apparent. They may also be
 CC used in this way to develop cell lines which remain viable in culture for
 CC an extended period. In contrast, if they act as cell death stimulators,
 CC Rbcl-y and Hbcl-y may be used to treat conditions associated with
 CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and
 CC lung cancer) and auto/hyperimmune diseases. They may also be used to
 CC cause cell death in, and hence control, parasites.
 XX
 XX Sequence 193 AA;
 SQ
 Query Match 98.3%; Score 992; DB 20; Length 193;
 Best Local Similarity 97.9%; Pred. No. 2.4e-100;
 Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MATPASTPDTRALVADFGVYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFTFRFRRT 60
 Db 1 MATPASAPDTRALVADFGVYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFTFRFRRT 60
 QY 61 FSDLAALQHLVTPGSAQQRFQVSDDELFOGGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 120
 Db 61 FSDLAALQHLVTPGSAQQRFQVSDDELFOGGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 120
 QY 121 QVQDMWVAYLETRLDADHSSGGNAEFTALYDGALEEARRLREGNWSVRTVLTGAVAL 180
 Db 121 QVQEMWVAYLETRLDADHSSGGNAEFTALYDGALEEARRLREGNWSVRTVLTGAVAL 180
 QY 181 GALVTVGGAFFASK 193
 Db 181 GALVTVGGAFFASK 193
 RESULT 8
 AAW36047
 ID AAW36047 standard; Protein; 193 AA.

XX AAW36047;
 AC
 XX 22-APR-1998 (first entry)
 DT
 XX Human bcl-w protein.
 DE
 XX
 XX Sci-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
 KW diagnosis; degenerative disease.
 KW
 XX Homo sapiens.
 OS
 XX WO9735971-A1.
 PN
 XX 02-OCT-1997.
 PD
 XX
 XX 27-MAR-1997; 97WO-AU00199.
 PF
 XX
 XX 27-MAR-1996; 96AU-0008965.
 PR
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA
 XX
 XX Adams JM, Cory S, Gibson LM, Holmgreen SP;
 PI
 XX WPI; 1997-489635/45.
 DR
 DR N-PSDB; AAT96577.
 XX
 XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce
 PT or inhibit cell survival, e.g. for treatment of cancer and
 CC degenerative diseases
 CC
 XX Claim 6; Page 48; 86pp; English.
 PS
 XX This sequence represents a novel human protein, bcl-w, encoded by the
 CC bcl-2 gene family and extracted from an adult brain library. This gene
 CC promotes cell survival, so its modulation is useful in treatment of
 CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,
 CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
 CC ischaemia, human immunodeficiency virus infection or in cell transplants.
 CC Up-regulation of the gene can also be used to modify cell lines cultured
 CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
 CC and to increase survival of primary explants during genetic modification.
 CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
 CC antibody production or screening of potential modulators.
 CC
 XX Sequence 193 AA;
 SQ
 Query Match 98.1%; Score 990; DB 18; Length 193;
 Best Local Similarity 97.4%; Pred. No. 4e-100;
 Matches 188; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MATPASTPDTRALVADFGVYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFTFRFRRT 60
 Db 1 MATPASAPDTRALVADFGVYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFTFRFRRT 60
 QY 61 FSDLAALQHLVTPGSAQQRFQVSDDELFOGGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 120
 Db 61 FSDLAALQHLVTPGSAQQRFQVSDDELFOGGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 120
 QY 121 QVQDMWVAYLETRLDADHSSGGNAEFTALYDGALEEARRLREGNWSVRTVLTGAVAL 180
 Db 121 QVQEMWVAYLETRLDADHSSGGNAEFTALYDGALEEARRLREGNWSVRTVLTGAVAL 180
 QY 181 GALVTVGGAFFASK 193
 Db 181 GALVTVGGAFFASK 193
 RESULT 9
 AAY05532
 ID AAY05532 standard; Protein; 193 AA.
 XX
 AC AAY05532;

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XX DT 05-JUL-1999 (first entry)
XX AC
XX XX
XX DT Human Bcl-w protein essential for spermatogenesis.
XX DE
XX KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
XX KW animal model.
XX OS Homo sapiens.
XX XX
XX PN WO9913710-A1.
XX XX
XX PD 25-MAR-1999.
XX PF
XX PF 16-SEP-1998; 98WO-AU00764.
XX PR
XX PR 16-SEP-1997; 97AU-0009228.
XX PA (HALL-; HALL INST MEDICAL RES WALTER & ELIZA.
XX PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
XX XX
XX DR WPI; 1999-243890/20.
XX DR N-PSDB; AAX25134.
XX XX
XX PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX PT protein associated with Bcl-w
XX PS Disclosure; Page 37; 52pp; English.
XX XX
XX CC The present sequence is described of a derivative of human Bcl-w
XX CC (see also AAK05301, a pro-survival member of the Bcl-2 family that
XX CC is widely expressed and which is essential for spermatogenesis.
XX CC The invention relates generally to a method of treatment and to an
XX CC animal model for the identification of molecules and genetic
XX CC sequences useful for inducing or reducing fertility of male animals.
XX CC Methods are provided for the treatment of infertility, or for
XX CC reducing fertility, by modulating spermatogenesis. An animal model
XX CC carries a mutation is at least one allele of the human or murine
XX CC bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w.
XX CC Such animals have disorganised seminiferous tubules and are
XX CC substantially infertile, but possess no other major abnormalities
XX CC as determined by histological examination. They can be used to
XX CC screen for therapeutic molecules including genetic sequences
XX CC capable of inducing, enhancing or otherwise facilitating
XX CC spermatogenesis in animals, or which can induce infertility.
XX XX
XX SQ Sequence 193 AA;
XX
XX Query Match 98.1%; Score 990; DB 20; Length 193;
XX Best Local Similarity 97.4%; Pred. No. 4e-100;
XX Matches 188; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1 MATPASTPDTALVADVGVYLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETFRRTF 60
Dy 1 MATPASAPDTALVADVGVYLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETFRRTF 60
Qy 61 FSDLAALQHLVTPGSAQORFTQVSDLELFGQGNWGRVLAFFVFGAALCAESVNKMEPLVG 120
Dy 61 FSDLAALQHLVTPGSAQORFTQVSDLELFGQGNWGRVLAFFVFGAALCAESVNKMEPLVG 120
Qy 121 QVQDMVMVAYLETRLDWIHSSGGWAEETALYDGALEEARLRGNWASVRTVLTGAVAL 180
Dy 121 QVQDMVMVAYLETRLDWIHSSGGWAEETALYDGALEEARLRGNWASVRTVLTGAVAL 180
Qy 181 GALVTVGAFPAASK 193
Dy 181 GALVTVGAFPAASK 193
XX
XX RESULT 10
XX AAW97394
XX ID AAW97394 standard; Protein; 192 AA.

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XX XX
XX AC AAW97394;
XX XX
XX DT 20-MAY-1999 (first entry)
XX DE
XX KW Mammalian bcl-y protein.
XX XX
XX KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
XX KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
XX KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
XX KW multiple sclerosis; myocardial infarction; vitally induced cell death;
XX KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
XX KW premature cell death; cell death stimulator; prolonged cell life span;
XX KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
XX XX
XX CS Mammalia.
XX XX
XX PN US5883229-A.
XX XX
XX PD 16-MAR-1999.
XX XX
XX PF 25-NOV-1997; 97US-0978523.
XX PR
XX PR 23-FEB-1996; 96US-0012201.
XX PR 11-FEB-1997; 97US-0798897.
XX PR 25-NOV-1997; 97US-0978523.
XX XX
XX PA (COCE-) COCENSYS INC.
XX XX
XX PI Guastella J;
XX DR WPI; 1999-214150/18.
XX XX
XX PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
XX PT for modulating programmed cell death
XX XX
XX PS Claim 2; Columns 19-22; 26pp; English.
XX XX
XX CC The present sequence represents a mammalian bcl-y protein.
XX CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
XX CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
XX CC thought to be involved in programmed cell death (apoptosis and necrosis).
XX CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
XX CC with a disruption of the cell death pathway. If they act as cell death
XX CC inhibitors, they may be used in therapies to treat subjects suffering
XX CC from strokes, head trauma, Alzheimer's Disease, neural and muscular
XX CC degenerative diseases (especially multiple sclerosis), myocardial
XX CC infarction, vitally induced cell death, aging, spinal cord injuries and
XX CC amyotrophic lateral sclerosis- conditions where cells under go premature
XX CC cell death as a result of triggers which may or may not be apparent.
XX CC They may also be used in this way to develop cell lines which remain
XX CC viable in culture for an extended period. In contrast, if they act as
XX CC cell death stimulators, Rbcl-y and Hbcl-y may be used to treat
XX CC conditions associated with prolonged cell life span such as cancer
XX CC (especially Kaposi's sarcoma and lung cancer) and auto/hyperimmune
XX CC diseases. They may also be used to cause cell death in, and hence
XX CC control, parasites.
XX XX
XX SQ Sequence 192 AA;
XX
XX Query Match 97.8%; Score 987; DB 20; Length 192;
XX Best Local Similarity 97.9%; Pred. No. 8.4e-100;
XX Matches 188; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 2 ATPASTPDTALVADVGVYLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETFRRTF 61
Dy 1 ATPASAPDTALVADVGVYLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETFRRTF 60
Qy 62 SOLAAQLHVTGSAQORFTQVSDLELFGQGNWGRVLAFFVFGAALCAESVNKMEPLVGQ 121
Dy 61 SOLAAQLHVTGSAQORFTQVSDLELFGQGNWGRVLAFFVFGAALCAESVNKMEPLVGQ 120

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QY 122 VQNMVAYLETRLDWTHSSGGWAEFTALYGDGALBEARLRREGNWSVTRVLTGAVALG 181
DB 121 VQNMVAYLETRLDWTHSSGGWAEFTALYGDGALBEARLRREGNWSVTRVLTGAVALG 180
QY 182 ALVTVGGAFFASK 193
DB 181 ALVTVGGAFFASK 192

RESULT 11
AAV05533
ID AAY05533 standard; Protein; 192 AA.
AC AAY05533;
XX
DT 05-JUL-1999 (first entry)
DE Mouse Bcl-w protein derivative.
XX

KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
animal model.

OS Mus sp.

EN WO9913710-A1.

PD 25-MAR-1999.

PF 16-SEP-1998; 98WO-AU00764.

PR 16-SEP-1997; 97AU-0009228.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

PI Adams J, Cory S, Gibson L, Koentgen F, Print C;

DR WPI; 1999-243890/20.

DR N-PSDB; AAX25135.

PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
protein associated with Bcl-w

PS Disclosure; Page 39; 52pp; English.

CC The present sequence is described of a derivative of mouse Bcl-w
(see also AAY05531), a pro-survival member of the Bcl-2 family that
is widely expressed and which is essential for spermatogenesis.
CC The derivative lacks the 24 N-terminal amino acids of Bcl-w.
CC The invention relates generally to a method of treatment and to an
animal model for the identification of molecules and genetic
sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for
reducing fertility, by modulating spermatogenesis. An animal model
carries a mutation is at least one allele of the human or murine
bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w.
CC Such animals have disorganised seminiferous tubules and are
substantially infertile, but possess no other major abnormalities
as determined by histological examination. They can be used to
screen for therapeutic molecules including genetic sequences
capable of inducing, enhancing or otherwise facilitating
spermatogenesis in animals, or which can induce infertility.

XX Sequence 192 AA;

Query Match 96.2%; Score 970.5; DB 20; Length 192;
Best Local Similarity 96.4%; Pred. No. 5.4e-98;
Matches 186; Conservative 4; Mismatches 2; Indels 1; Gaps 2;

QY 1 MATPASTPDTALVADFVGYRLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MPTPASTPDTALVADFVGYRLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAALQHLVTFGSAQQORFTQVSDLELFOGGPNWGRLVAFVFGAALCAESVKNEMEPLVG 120

DB 61 FSDLAALQHLVTFGSAQQORFTQVSDLELFOGGPNWGRLVAFVFGAALCAESVKNEMEPLVG 120
QY 121 QVCDNMVAYLETRLDWTHSSGGWAEFTALYGDGALBEARLRREGNWSVTRVLTGAVAL 180
DB 121 QVCDNMVAYLETRLDWTHSSGGWAEFTALYGDGALBEARLRREGNWSVTRVLTGAVAL 179
QY 181 GALVTVGGAFFASK 193
DB 180 GALVTVGGAFFASK 192

RESULT 12

AAW36048

CD AAW36048 standard; Protein; 168 AA.

AC AAW36048;

XX

DT 22-APR-1998 (first entry)

DE Mouse bcl-w protein.

XX

KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;

diagnosis; degenerative disease.

OS Mus sp.

PN WO9735971-A1.

PD 02-OCT-1997.

PF 27-MAR-1997; 97WO-AU00199.

PR 27-MAR-1996; 96AU-0008965.

PA (AMSA-) AMRAD OPERATIONS PTY LTD.

PI Adams JM, Cory S, Gibson LM, Holmgren SP;

DR WPI; 1997-489635/45.

DR N-PSDB; AAT96578.

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce

or inhibit cell survival, e.g. for treatment of cancer and

degenerative diseases

PS Claim 6; Page 50-51; 86pp; English.

CC This sequence represents a novel protein, bcl-w, encoded by the mouse
bcl-2 gene family. This gene promotes cell survival, so its modulation
is useful in treatment of cancer or auto-immune diseases, degenerative
diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular
degeneration, hypoxia, ischaemia, human immunodeficiency virus infection
or in cell transplants. Up-regulation of the gene can also be used to
modify cell lines cultured in vivo, e.g. to develop new lines, to
facilitate isolation of hybridomas and to increase survival of primary
explants during genetic modification. It can be used to produce
recombinant Bcl-w for therapy, diagnosis, antibody production or
screening of potential modulators.

XX Sequence 168 AA;

Query Match 87.1%; Score 879; DB 18; Length 168;
Best Local Similarity 87.6%; Pred. No. 4.8e-88;
Matches 164; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDTALVADFVGYRLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MPTPASTPDTALVADFVGYRLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAALQHLVTFGSAQQORFTQVSDLELFOGGPNWGRLVAFVFGAALCAESVKNEMEPLVG 120
DB 61 FSDLAALQHLVTFGSAQQORFTQVSDLELFOGGPNWGRLVAFVFGAALCAESVKNEMEPLVG 120

```

QY 121 QVQDMVAYLETRLADWIHSSGGWAEFTALYDGALEEARLRREGNWA 168
DB 121 QVQDMVAYLETRLADWIHSSGGWAEFTALYDGALEEARLRREGNWA 168

RESULT 13
AAO18223
ID AAO18223 standard; Protein; 190 AA.
XX
XX AAO18223;
XX
XX 18-SEP-2002 (first entry)
XX
XX Human Bcl-Rambo BHNO domain related protein #4.
XX Human; apoptotic signal transduction protein; Bcl-Rambo; BHNO domain;
XX cancer; neurodegenerative disease; Alzheimer's disease; cytostatic;
XX neurotropic; neuroprotective; antiparkinsonian; virucide; antiinflammatory;
XX immunosuppressive; anti-HIV; antibacterial; hepatotropic; septic shock;
XX Parkinson's disease; muscular dystrophy; HIV; viral infection; hepatitis;
XX graft versus host disease; autoimmune disease.
XX
XX Unidentified.
XX
XX WO200248353-A2.
XX
XX 20-JUN-2002.
XX
XX 12-DEC-2001; 2001WO-EP14597.
XX
XX 12-DEC-2000; 2000DE-1061766.
XX
XX 04-JAN-2001; 2001DE-1000280.
XX
XX (APOT-) APOTECH RES & DEV LTD.
XX
XX Tschopp J, Hofmann K;
XX
XX WPI; 2002-537627/57.
XX
XX New DNA encoding Bcl-Rambo protein, useful for treating e.g. tumors and
XX for identifying therapeutic modulators of Bcl-Rambo function -
XX
XX Disclosure; Fig 1: 6lpp; German.
XX
XX The present invention provides the protein and coding sequences of the
XX human Bcl-Rambo apoptotic transcription factor, particularly the BHNO
XX domain. The sequences are useful in the treatment of diseases caused by
XX incorrectly regulated intracellular signal transduction, including
XX cancers, neurodegenerative diseases (e.g. Alzheimer's or Parkinson's
XX diseases), muscular dystrophy, viral infections (including human
XX immunodeficiency virus), autoimmune disease, septic shock, graft versus
XX host disease and acute hepatitis. The present sequence is a protein
XX described in the exemplification of the invention.
XX
XX Sequence 190 AA;
XX
XX Query Match 80.4%; Score 811.5; DB 23; Length 190;
XX Best Local Similarity 86.5%; Pred. No. 1.4e-80;
XX Matches 167; Conservative 2; Mismatches 2; Indels 3; Gaps 3;
XX
QY 1 MATPASTPTDTRALVADFVGYRLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASAPTXAXVAD-XGYLRLQKGYVNGAGPGGPAAD-XHQAXAAGKEFETRFRRT 58
QY 61 FSDLAQLHVTTPGSAQORFTQVSDSELFQGGPNWGRLVAFVFGAALCAESVKNKEPLVG 120
DB 59 FSDLAQLHVTTPGSAQORFTQVSDSELFQGXNWXGXAXFAFFVFGAAXCAESVKNKEPLVG 118
QY 121 QVQDMVAYLETRLADWIHSSGGWAEFTALYDGALEEARLRREGNWA 168
DB 119 QVQDMVAYLETX-AX-IHSSGGWAEFTALYDGALEEARLRREGNWA 177

QY 181 GALVTVGAFPAASK 193
DB 178 GALVTVGAFPAASK 190

RESULT 14
AAW59884
ID AAW59884 standard; Protein; 365 AA.
XX
XX AAW59884;
XX
XX 20-NOV-1998 (first entry)
XX
XX Amino acid sequence of the cDNA clone Bcl-like (HAICH29).
XX Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
XX immunological disorder; autoimmune disease; anti-infectious agent.
XX
XX Homo sapiens.
XX
XX WC9831800-A2.
XX
XX 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US00960.
XX
XX 21-JAN-1997; 97US-0034205.
XX
XX 21-JAN-1997; 97US-0034204.
XX
XX (AUCK-) AUCKLAND UNISERVICES LTD.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA;
XX Su JY;
XX
XX WEI; 1998-414059/35.
XX
XX N-PSDB; AAV41925.
XX
XX New isolated polynucleotides and encoded polypeptides - used to
XX develop products for treating e.g. inflammatory diseases,
XX infections, immunological disorders, autoimmune diseases, allergies
XX or tumors
XX
XX Claim 1; Fig 12A-12D; 120pp; English.
XX
XX This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29),
XX used in the method of the invention. The products of the clone can be
XX used for treating conditions associated with abnormal expression of
XX the polypeptides. They can be used for e.g. treating chronic
XX inflammatory diseases, immunological disorders, autoimmune diseases,
XX inflammatory diseases, varicous allergies, and as anti-infectious agents.
XX The products can also be used for detection and diagnosis.
XX
XX Sequence 365 AA;
XX
XX Query Match 74.9%; Score 756; DB 19; Length 365;
XX Best Local Similarity 97.9%; Pred. No. 4.2e-74;
XX Matches 141; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 MATPASTPTDTRALVADFVGYRLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASAPTXAXVAD-XGYLRLQKGYVNGAGPGGPAAD-XHQAXAAGKEFETRFRRT 60
QY 61 FSDLAQLHVTTPGSAQORFTQVSDSELFQGGPNWGRLVAFVFGAALCAESVKNKEPLVG 120
DB 61 FSDLAQLHVTTPGSAQORFTQVSDSELFQGGPNWGRLVAFVFGAALCAESVKNKEPLVG 120
QY 121 QVQDMVAYLETRLADWIHSSGGW 144
DB 121 QVQDMVAYLETRLADWIHSSGGW 144

RESULT 15

```


ABG95556
 ID ABG95556 standard; Protein; 365 AA.
 XX
 AC ABG95556;
 XX
 DT 15-JAN-2003 (first entry)
 XX
 DE Human novel secreted protein gene 120 polypeptide #1.
 XX
 KW Human: secreted protein; autoimmune disease; chemotaxis;
 KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasia;
 KW liver neoplasia cardiovascular disorder; cardiac arrest; skin aging;
 KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
 KW nervous system disorders; Alzheimer's disease; infection;
 KW ocular disorder; corneal infection; wound healing; tissue regeneration;
 KW epithelial cell proliferation; organ transplantation; food additive;
 KW preservative; nutritional.
 XX
 OS Homo sapiens.
 XX
 PN US6420526-B1.
 XX
 PD 16-JUL-2002.
 XX
 PF 08-SEP-1998; 98US-0149476.
 XX
 PR 07-MAR-1997; 97US-038621P.
 PR 07-MAR-1997; 97US-040161P.
 PR 07-MAR-1997; 97US-040162P.
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 PR 11-APR-1997; 97US-043311P.
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 PR 23-MAY-1997; 97US-047501P.
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 PR 06-JUN-1997; 97US-048864P.
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 PR 13-JUN-1997; 97US-049610P.
 PR 08-JUL-1997; 97US-051326P.
 PR 16-JUL-1997; 97US-052874P.
 PR 18-AUG-1997; 97US-055724P.
 PR 22-AUG-1997; 97US-056630P.
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 PR 22-AUG-1997; 97US-056884P.
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 PR 22-AUG-1997; 97US-056903P.
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 PR 05-SEP-1997; 97US-057650P.
 PR 05-SEP-1997; 97US-057669P.
 PR 12-SEP-1997; 97US-058785P.
 PR 02-OCT-1997; 97US-061060P.
 PR 05-MAR-1998; 98WO-US04493.
 XX
 XX (HUYA-); HUMAN GENOME SCI INC.
 PA
 XX
 XX
 PI Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarik DR;
 PI Erdress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
 PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
 P: Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
 XX
 XX WPI; 2002-634796/68.
 DR
 XX
 XX
 PT New isolated human secreted protein for diagnosing, preventing,
 PT treating or ameliorating medical conditions and used as a food additive
 PT or preservative
 XX
 PS Disclosure; Column 103; 129pp; English.
 XX
 CC The invention relates to an isolated protein that is one of 186 human
 CC secreted proteins, given in the specification, encoded by one of
 CC 309 cDNA sequences also given in the specification. The protein is used

Search completed: October 24, 2003, 10:48:55
Job time : 61 secs

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OM protein - protein search, using sw model

Run on: October 24, 2003, 10:46:25 ; Search time 21 Seconds

(without alignments)

388.857 Million cell updates/sec

Title: US-09-925-674A-9

Perfect score: 1009

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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/prodata/2/aaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/2/aaa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/2/aaa/PCITUS_COMB.pep.*
- 6: /cgn2_6/prodata/2/aaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1002	99.3	193	1	US-08-798-897-3
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3	997	98.8	192	1	US-08-798-897-5
4	997	98.8	192	2	US-08-978-523-5
5	992	98.3	193	1	US-08-798-897-4
6	992	98.3	193	2	US-08-978-523-4
7	987	97.8	192	1	US-08-798-897-6
8	987	97.8	192	2	US-08-978-523-6
9	756	74.9	365	4	US-09-149-476-696
10	425.5	42.2	233	4	US-09-271-014A-6
11	424.5	42.1	233	1	US-08-333-565-59
12	424.5	42.1	233	1	US-08-081-448-6
13	424.5	42.1	233	1	US-08-607-268-24
14	424.5	42.1	233	1	US-08-471-058-14
15	424.5	42.1	233	2	US-08-662-479-59
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20	424.5	42.1	233	3	US-09-323-743-2
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24	424.5	42.1	233	5	PCT-US95-04600-24
25	422	41.8	225	3	US-09-101-519-1
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28	409	40.5	236	1	US-08-607-269-22
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45	406.5	40.3	239	2	US-08-661-479-51

ALIGNMENTS

RESULT 1

US-08-798-897-3
; Sequence 3, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-798-897-3

Query Match 99.3%; Score 1002; DB 1; Length 193;
Best Local Similarity 99.0%; Pred. No. 3.3e+106;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTETRALVADFGVRLQKGYVCGAGPGGPAADPLHQAAMRAAGDEFETRFRRT 60

DB 1 MATPASTPTETRALVADFGVRLQKGYVCGAGPGGPAADPLHQAAMRAAGDEFETRFRRT 60

QY 61 FSDLAALQHLVTPGSAQRFTQVSDLFQGGPNWGRVLAFFVFGAALCAESVNMKEPLVG 120

Db 61 FSDLAQLHVTFGSAQQRFTQVSDLEFQGGNWRGLVAFVFGAALCAESVKNEMEPLVG 120
QY 121 QVQDMWVYLETRLADWIHSSGGWAEFTALYGDGALBEARLRREGNWSVRTVLTGAVAL 180
Db 121 QVQDMWVYLETRLADWIHSSGGWAEFTALYGDGALBEARLRREGNWSVRTVLTGAVAL 180
QY 181 GALVTGGAFFASK 193
Db 181 GALVTGGAFFASK 193
RESULT 2
US-08-978-523-3
; Sequence 3, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978.523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-978-523-3
Query Match 99.3%; Score 1002; DB 2; Length 193;
Best Local Similarity 99.0%; Pred. No. 3.3e-106;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MATPASTPDTRALVADFGYGLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFTFRRTF 60
Db 1 MATPASTPDTRALVADFGYGLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFTFRRTF 60
QY 61 FSDLAQLHVTFGSAQQRFTQVSDLEFQGGNWRGLVAFVFGAALCAESVKNEMEPLVG 120
Db 61 FSDLAQLHVTFGSAQQRFTQVSDLEFQGGNWRGLVAFVFGAALCAESVKNEMEPLVG 120
QY 121 QVQDMWVYLETRLADWIHSSGGWAEFTALYGDGALBEARLRREGNWSVRTVLTGAVAL 180
Db 121 QVQDMWVYLETRLADWIHSSGGWAEFTALYGDGALBEARLRREGNWSVRTVLTGAVAL 180

QY 181 GALVTGGAFFASK 193
Db 181 GALVTGGAFFASK 193
RESULT 3
US-08-798-897-5
; Sequence 5, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-798-897-5
Query Match 98.8%; Score 997; DB 1; Length 192;
Best Local Similarity 99.0%; Pred. No. 1.2e-105;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 ATPASTPDTRALVADFGYGLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFTFRRTF 61
Db 2 ATPASTPDTRALVADFGYGLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFTFRRTF 60
QY 62 SDLAALHVTFGSAQQRFTQVSDLEFQGGNWRGLVAFVFGAALCAESVKNEMEPLVG 121
Db 61 SDLAALHVTFGSAQQRFTQVSDLEFQGGNWRGLVAFVFGAALCAESVKNEMEPLVG 120
QY 122 VQDMWVYLETRLADWIHSSGGWAEFTALYGDGALBEARLRREGNWSVRTVLTGAVAL 181
Db 121 VQDMWVYLETRLADWIHSSGGWAEFTALYGDGALBEARLRREGNWSVRTVLTGAVAL 180
QY 182 ALVTGGAFFASK 193
Db 181 ALVTGGAFFASK 192
RESULT 4
US-08-978-523-5
; Sequence 5, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John

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STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-03-798-897-4

Query Match 98.3%; Score 992; DB 1; Length 193;
Best Local Similarity 97.9%; Pred. No. 4.5e-105;
Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASPTDTRALVADVGVRLRQKGYVCGAGPGGPAADPLHQAMRAAGDEPETRFRRT 6C
Db 1 MATPASAPDTRALVEDFVGKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEPETRFRRT 60
QY 61 PSDLAALQHLVTPGSAQORFTQVSDELFOGQPNWGLVAFVFGAALCAESVNKEMEPLVG 120
Db 61 PSDLAALQHLVTPGSAQORFTQVSDELFOGQPNWGLVAFVFGAALCAESVNKEMEPLVG 120
QY 121 QVODMWVAYLETRADWIHSSGWAEEFTALYGDGALEEARLRREGNWSVTVLTGAVAL 180
Db 121 QVQDWMVAYLETRADWIHSSGWAEEFTALYGDGALEEARLRREGNWSVTVLTGAVAL 180
QY 181 GALVTGGAFFASK 193
Db 181 GALVTGGAFFASK 193

RESULT 6
US-08-978-523-4
Sequence 4, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith

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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-978-523-4

Query Match      98.3%; Score 992; DB 2; Length 193;
Best Local Similarity 97.9%; Pred. No. 4.5e-105;
Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASTPTTRALVADFGYRLRQKGYVCGAGPGGPAADPLHQMRAAGDEFEFTRRTF 60
DB 1 MATPASPOTRALVEDFGYKLRQKGYVCGAGPGGPAADPLHQMRAAGDEFEFTRRTF 60
QY 61 FSDLAQLHVTGSAQQRFTQVSDQLFQGGPNWGRVLAFFVFGAALCAESVNKEMEPLVG 120
DB 61 FSDLAQLHVTGSAQQRFTQVSDQLFQGGPNWGRVLAFFVFGAALCAESVNKEMEPLVG 120
QY 121 QVQDMWVAYLETRLDWTHSSGGAETALYCDGALBEARLRGNWASVRTVLTGVAL 180
DB 121 QVQDMWVAYLETRLDWTHSSGGAETALYCDGALBEARLRGNWASVRTVLTGVAL 180
QY 181 GALVTGGAFFASK 193
DB 181 GALVTGGAFFASK 193

RESULT 7
US-08-798-897-6
; Sequence 6, Application US/08798857
; Patent No. 5785201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
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; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-798-897-6

Query Match      97.8%; Score 987; DB 1; Length 192;
Best Local Similarity 97.9%; Pred. No. 1.7e-104;
Matches 188; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATPASTPTTRALVADFGYRLRQKGYVCGAGPGGPAADPLHQMRAAGDEFEFTRRTF 61
DB 1 ATPASPOTRALVEDFGYKLRQKGYVCGAGPGGPAADPLHQMRAAGDEFEFTRRTF 60
QY 62 SDLAQLHVTGSAQQRFTQVSDQLFQGGPNWGRVLAFFVFGAALCAESVNKEMEPLVG 120
DB 61 SDLAQLHVTGSAQQRFTQVSDQLFQGGPNWGRVLAFFVFGAALCAESVNKEMEPLVG 120
QY 122 QVQDMWVAYLETRLDWTHSSGGAETALYCDGALBEARLRGNWASVRTVLTGVAL 181
DB 121 QVQDMWVAYLETRLDWTHSSGGAETALYCDGALBEARLRGNWASVRTVLTGVAL 180
QY 182 ALVTGGAFFASK 193
DB 181 ALVTGGAFFASK 192

RESULT 8
US-08-978-523-6
; Sequence 6, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-08-978-523-6
Query Match 97.8%; Score 987; DB 2; Length 192;
Best Local Similarity 97.9%; Fred. No. 1.7e-104;
Matches 188; Conservative 2; Mismatches 2; Indels 0; Gaps 3;

QY 2 ATPASPTDRALVADVGVRALQKGVYCGAGGEGPAADPLHQAVRAAGDEFETFRRTTF 61
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1 ATPASAPDTRALVEDVGVKZLKQKGVYCGAGGEGPAADPLHQAVRAAGDEFETFRRTF 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 62 SOLAAQLHVTGPSACQRFQVSDQLFQGGPMGRVLVAFVFGAALCAESVKNKMEP-VGQ 121
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 122 VQWMMVAYLETRLADNHSSGWAEBETALYDGCALBEPRLREGNWSVRTLGAVALG 181
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 VQWMMVAYLETRLADNHSSGWAEBETALYDGCALBEPRLREGNWSVRTLGAVALG 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 182 ALVTVGGAFFASK 193
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 ALVTVGGAFFASK 192
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
US-09-149-476-696
; Sequence 696, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human. Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,562
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,920
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,364
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
Query Match 74.9%; Score 756; DB 4; Length 365;
Best Local Similarity 97.9%; Pred. No. 8.9e-78;
Matches 141; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY : MATPASTEDTRALVADFVGYKLRQGVYCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASAFDTRALVADFVGYKLRQGVYCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAALQHVTPGSAQORFTQVSDLEFQGGNMGRLVAFVFGAALCAESVNKEPELVG 120
DB 61 FSDLAALQHVTPGSAQORFTQVSDLEFQGGNMGRLVAFVFGAALCAESVNKEPELVG 120
QY 121 QVQDMVMVAYLETRLADWIHSSGGW 144
DB 121 QVQDMVMVAYLETRLADWIHSSGGW 144
RESULT 10
US-09-271-014A-6
Sequence 6, Application US/09271014A
Patent No. 6395510
GENERAL INFORMATION:
APPLICANT: THOMPSON, CRAIG B.
APPLICANT: BOISE, LAWRENCE H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:316
CURRENT APPLICATION NUMBER: US/09/271,014A
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 233
TYPE: PRT
ORGANISM: Human
US-09-271-014A-6
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Best Local Similarity 40.6%; Pred. No. 2.1e-40;
Matches 91; Conservative 24; Mismatches 59; Indels 51; Gaps 4;
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DB 6 RELVDFLSYKLSQKGYSMQFSQVDEENRTEAPEGTGSEMETPSAINGNPSMHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFETRFRRTFSDLAALQHVTPGSAQORFTQ 81
DB 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRAFSDL*SQLHITGTAYQSFEQ 125
QY 82 VSEDFQGGNMGRLVAFVFGAALCAESVNKEPELVGQVQDMVMVAYLETRLADWIHSS 141
DB 126 VVNEUFRDGVNMGRIVAFPSFGALCVESVKEMOVLVSRIAAMWATYLNCHLEPWIQEN 185
QY 142 GQWAEFTALYGDGALEEARLRE--GNWASRTVLTGVALGAL 183
DB 186 GQWDTFVELYGNNAASRKQGERENRWFELTGMTVAGVVLGSL 229
RESULT 11
US-08-333-565-59
Sequence 59, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR


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; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,565
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
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; US-08-333-565-59
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; Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 4;
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; DB 185 NGWDTFVELYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229
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; RESULT 12
; US-08-081-448-6
; Sequence 6, Application US/08081448
; Patent No. 5646008
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5646008th Clark Street, Suite 800
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; FILING DATE: 19930622
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646008thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-744-0090
; TELEFAX: 312-755-4489
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: pro-ein
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; Query Match 42.1%; Score 424.5; DB 1; Length 233;
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; Matches 90; Conservative 24; Mismatches 59; Indels 51; Gaps 4;
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; QY 82 VDELFGGPNWGRVAVFFVFGAALCAESVKNKMEPLVGVQVDMVMVAYLETRLADWIHS 141
; DB 126 VVNNELFRDGVNMGRIVAFFSFGALCVESVDKEMQVLSRIAAMWATYLNHLEPWIQE 185
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; QY 142 GWAAEFTALYDGALEEARLRE--GNWASVRTVLTGAVALGAL 183
; DB 186 GGDWTFVELYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229
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; RESULT 13
; US-08-607-269-24
; Sequence 24, Application US/08607269
; Patent No. 5702897
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: Interaction of Proteins Involved in a
; TITLE OF INVENTION: Cell Death Pathway
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/607,269
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/226,876
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9892
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-607-269-24

Query Match 42.1%; Score 424.5; DB 1; Length 233;
Best Local Similarity 40.2%; Pred. No. 2.7e-40;
Matches 90; Conservative 24; Mismatches 59; Indels 51; Gaps 4;
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DB 6 RELVDFLSYKLSQGYWSQFSQFSEVNRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65
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DB 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLSHITPGTAYQSFQ 125
QY 82 VSDLEFGGPNMGRIVAFFFGAALCAESVNKEPELVGQVQDWMVAYLETRLADWHSS 141
DB 126 VVNELFDDGVNMGRIVAFFFGGALCVESVDKENVLVSRAAWMATYLNHDLSEFWICE 185
QY 142 GGMAEFTALYGDGALEBARLRB--GNWASVRTVLTGAVALGAL 183
DB 186 GGWDTFVELYGNNAAESRKQGRFNRMTGTMTVAGVVLGSL 229

RESULT 14
US-08-471-058-14
Sequence 14, Application US/08471058
Patent No. 5770443
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792

TELEX: 706141
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 40.9%; Pred. No. 2.7e-40;
Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 4;
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DB 6 RELVDFLSYKLSQGYWSQFSQFSEVNRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65
QY 29 CGAGCEGCPAAD-----PLHQAMRAAGDEFETFRRTFSDLAQAQLHVTGSAQOQFT 80
DB 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLSHITPGTAYQSFQ 124
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RESULT 15
US-08-661-473-59
Sequence 59, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-661-473-59

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Query Match.      42.1%; Score 424.5; DB 2; Length 233;
Best Local Similarity 40.9%; Pred. No. 2.7e-40;
Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 4;

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Search completed: October 24, 2003, 10:52:52
Job time : 22 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: October 24, 2003, 10:51:15 ; Search time 45.5 Seconds
(without alignments)
710.328 Million cell updates/sec

Title: US-09-925-674A-9
Perfect score: 100%
Sequence: 1 MATPASTPTDTRALVADFVGY.....JGVALGALVTVGAFPPASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	997	98.8	193	10	US-09-925-674A-7 Sequence 7, Appl
3	756	74.9	365	11	US-09-809-391-696 Sequence 696, App
4	756	74.9	365	12	US-09-882-171-696 Sequence 696, App
5	424.5	42.1	233	9	US-09-734-846-2 Sequence 2, Appl
6	424.5	42.1	233	10	US-09-952-278-6 Sequence 6, Appl
7	424.5	42.1	233	12	US-10-169-223-10 Sequence 10, App
8	424.5	42.1	233	12	US-10-302-262-2 Sequence 2, Appl
9	424.5	42.1	233	15	US-10-101-482-14 Sequence 14, App
10	424.5	42.1	233	15	US-10-072-830-4 Sequence 4, Appl
11	411.5	40.8	152	15	US-10-158-769-2 Sequence 2, Appl
12	408.5	40.3	239	5	US-10-277-693A-10 Sequence 10, App
13	406.5	40.3	239	8	US-08-726-211-5 Sequence 5, Appl
14	406.5	40.3	239	12	US-10-141-618-12 Sequence 12, App
15	406.5	40.3	239	12	US-10-053-645A-21 Sequence 21, Appl

16	406.5	40.3	239	15	US-10-101-482-12	Sequence 12, Appl
17	406.5	40.3	239	15	US-10-072-830-2	Sequence 2, Appl
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24	342	33.9	205	8	US-08-726-211-7	Sequence 7, Appl
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26	342	33.9	205	12	US-10-053-645A-23	Sequence 23, Appl
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33	174	17.2	211	15	US-10-177-293-25	Sequence 25, Appl
34	169	16.7	211	15	US-10-101-482-9	Sequence 9, Appl
35	169	16.7	211	15	US-10-101-482-11	Sequence 11, Appl
36	166.5	16.5	210	15	US-10-101-482-22	Sequence 22, Appl
37	156.5	15.5	192	15	US-10-277-693A-8	Sequence 8, Appl
38	154	15.3	191	15	US-10-196-793A-46	Sequence 46, Appl
39	154	15.3	192	12	US-10-306-878-5	Sequence 5, Appl
40	154	15.3	192	15	US-10-101-482-13	Sequence 13, Appl
41	154	15.3	192	15	US-10-277-693A-9	Sequence 9, Appl
42	154	15.3	280	15	US-10-101-482-19	Sequence 19, Appl
43	154	15.3	331	9	US-09-033-525-2	Sequence 2, Appl
44	153	15.2	192	15	US-10-277-693A-2	Sequence 2, Appl
45	153	15.2	212	12	US-10-299-514A-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-925-674A-9
; Sequence 9, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925.674A
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: P08965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mouse
US-09-925-674A-9

Query Match	100.0%	Score	1009	DB	10	Length	193
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/047,582
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; PRIOR APPLICATION NUMBER: 60/048,974
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; PRIOR APPLICATION NUMBER: 60/056,888
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,879
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,880
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,894
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,911
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,636

;
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,874
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,910
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,864
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,631
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,892
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,761
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/047,595
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,588
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,585
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,586
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,590
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Query Match 74.9%; Score 756; DB 12; Length 365;
Best Local Similarity 97.9%; Pred. No. 1.4e-73;
Matches 141; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MATPASTEDTRALVADVGVYRLKQGVYCCGPGEGFADPLHCAMRAAGDEFTFRFT 60
Db 1 MATPASAPDTRALVADVGVYKLRKQGVYCCGPGEGFADPLHCAMRAAGDEFTFRFT 60
QY 61 FSDLAQLHVTGPSAQORFTQVSDLEFQGGPNMGRLVAFVFGAALCAESVNKEMEPLVG 120
Db 61 FSDLAQLHVTGPSAQORFTQVSDLEFQGGPNMGRLVAFVFGAALCAESVNKEMEPLVG 120
QY 121 QVQDMVAYLETRLADWIHSSGGW 144
Db 121 QVQDMVAYLETRLADWIHSSGGW 144

RESULT 5
US-09-734-846-2
; Sequence 2, Application US/09734846
; Patent No. US20010007025A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0528
; CURRENT APPLICATION NUMBER: US/09/734,846
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/323,743
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-734-846-2

Query Match 42.1%; Score 424.5; DB 9; Length 233;
Best Local Similarity 40.2%; Pred. No. 7.5e-36;
Matches 90; Conservative 24; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADVGVYRLKQGY-----VCGAGP-----GEGPAA 39
Db 6 RELVDFLSYKLSQKGYSWQSFSDVENRTEAPGTESEMETPSAINGNPSWHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFTFRFTFSDLAQLHVTGPSAQORFTQ 81
Db 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFFELRYVRA=SDLTSQLHITPGTAYQSEFQ 125
QY 82 VSDLEFQGGPNMGRLVAFVFGAALCAESVNKEMEPLVGQVQDMVAYLETRLADWIHSS 141
Db 126 VYNELFRDGVNMGRIVAFVFGGALCVESVDKENQVLVSRIAAMMATYLNHLEPFIQEN 185
QY 142 GGMAEFTALYGDGALAEARLRE--GYNASVRTVLTCGAVLGAAL 183
Db 186 GGMDFVELYGNNAAESRKQGRFNRLTGMTVAGVVLGSL 229

RESULT 6
US-09-952-278-6
; Sequence 6, Application US/09952278
; Patent No. US20020137182A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: Vertebate Apoptosis Gene:
; NUMBER OF SEQUENCES: 8
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. US20020137182A1th Clark Street, Suite 800
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/952,278
; FILING DATE: 12-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,448
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020137182A1thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-744-0090
; TELEFAX: 312-755-4489
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-952-278-6

Query Match 42.1%; Score 424.5; DB 10; Length 233;
Best Local Similarity 40.2%; Pred. No. 7.5e-38;
Matches 90; Conservative 24; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADVGVYRLKQGY-----VCGAGP-----GEGPAA 39
Db 6 RELVDFLSYKLSQKGYSWQSFSDVENRTEAPGTESEMETPSAINGNPSWHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFTFRFTFSDLAQLHVTGPSAQORFTQ 81
Db 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFFELRYVRA=SDLTSQLHITPGTAYQSEFQ 125
QY 82 VSDLEFQGGPNMGRLVAFVFGAALCAESVNKEMEPLVGQVQDMVAYLETRLADWIHSS 141
Db 126 VYNELFRDGVNMGRIVAFVFGGALCVESVDKENQVLVSRIAAMMATYLNHLEPFIQEN 185
QY 142 GGMAEFTALYGDGALAEARLRE--GYNASVRTVLTCGAVLGAAL 183
Db 186 GGMDFVELYGNNAAESRKQGRFNRLTGMTVAGVVLGSL 229

RESULT 7
US-10-169-223-10
; Sequence 10, Application US/10169223
; Publication No. US20030152946A1
; GENERAL INFORMATION:
; APPLICANT: SHIMIZU, Shigeomi
; APPLICANT: TSUJIMOTO, Yoshihide
; TITLE OF INVENTION: BH4-Fused Polypeptides
; FILE REFERENCE: 1422-0537P
; CURRENT APPLICATION NUMBER: US/10/169,223
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: JP 11-371449
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: PCT/JP00/09274
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.1
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; SEQ ID NO 10
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-169-223-10

Query Match
  42.1%; Score 424.5; DB 12; Length 233;
Best Local Similarity 40.2%; Pred. No. 7.5e-38;
Matches 90; Conservative 24; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADFVGYRLQKGY-----VCGAGP-----GEGPAA 39
DB 6 RELVDFLSYKLSQKGYSWQSFSDVENRTEAPEGTSEMETPSAINGNPSWHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFFETRRRTFSDLAALQHLVTPGSAQQRFTQ 91
DB 66 NGATAHSSSLDAREVIPAAMVKQALREAGDEFFELRYRRAFSDLTSLQHLITPGTAYQSFE 125
QY 82 VSDLEFGGPNWGLVAFVFGAALCAESVKNKEPVLGVQVQDMVAYLETRLDWIHS 141
DB 126 VNNEFLPDGVNMGRIVAFFSFGGALCVESVDKEMQVLVSRIAAMVATYLNHLEPWIQEN 185
QY 142 GGWAETALYDGALEEARLRE--GNWASVRTVLTGAVALGAL 183
DB 186 GGWDTFVELYGNNAAESRKQGRFNRWFLTGMTVAGVLLGSL 229

RESULT 8
US-10-302-262-2
; Sequence 2, Application US/1C3C2262
; Publication No. US20030191300A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0528
; CURRENT APPLICATION NUMBER: US/10/302,262
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/734,846
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/323,743
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-302-262-2

Query Match
  42.1%; Score 424.5; DB 12; Length 233;
Best Local Similarity 40.2%; Pred. No. 7.5e-38;
Matches 90; Conservative 24; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADFVGYRLQKGY-----VCGAGP-----GEGPAA 39
DB 6 RELVDFLSYKLSQKGYSWQSFSDVENRTEAPEGTSEMETPSAINGNPSWHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFFETRRRTFSDLAALQHLVTPGSAQQRFTQ 91
DB 66 NGATAHSSSLDAREVIPAAMVKQALREAGDEFFELRYRRAFSDLTSLQHLITPGTAYQSFE 125
QY 82 VSDLEFGGPNWGLVAFVFGAALCAESVKNKEPVLGVQVQDMVAYLETRLDWIHS 141
DB 126 VNNEFLPDGVNMGRIVAFFSFGGALCVESVDKEMQVLVSRIAAMVATYLNHLEPWIQEN 185

; SEQ ID NO 10
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-101-482-14

Query Match
  42.1%; Score 424.5; DB 15; Length 233;
Best Local Similarity 40.9%; Pred. No. 7.5e-38;
Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADFVGYRLQKGY-----V 28
DB 6 RELVDFLSYKLSQKGYSWQSFSDVENRTEAPEGTSEMETPSAINGNPSWHLADSPAV 65
QY 29 CGAGPGECPAAD-----PLHQAMRAAGDEFFETRRRTFSDLAALQHLVTPGSAQQRFT 80
DB 66 NGA-TGHSSSLDAREVIPAAMVKQALREAGDEFFELRYRRAFSDLTSLQHLITPGTAYQSFE 124
QY 81 QVSDLEFGGPNWGLVAFVFGAALCAESVKNKEPVLGVQVQDMVAYLETRLDWIHS 140
DB 125 QVNNEFLPDGVNMGRIVAFFSFGGALCVESVDKEMQVLVSRIAAMVATYLNHLEPWIQ 184
QY 141 SGWAETALYDGALEEARLRE--GNWASVRTVLTGAVALGAL 183
DB 185 NGGMDTFVELYGNNAAESRKQGRFNRWFLTGMTVAGVLLGSL 229

RESULT 10
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Matches 79; Conservative 18; Mismatches 45; Indels 9; Gaps 1
QQY      11 RALVAQFVGVRQRKGVCV-----AGEGEPAADPLHQAVRAAGDEFETRRTTF 61
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Ddb       2 RELVDWFLSKLQSGYSQSFDVEENRTEAPECTESEAVKQALREAGDEFELRVRAF 61
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
QQY      62 SDLAALQLHTVPGSAQGRFTQVSDELFOGGPNWGRLVAFVFGAALCAESVNKEVEPLVG 121
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Ddb       62 SDLTSLQHITPQTAYOSPFQVVNELFRDGVNMGRIVAFPSFGALCVESVDKEXVLVSR 121
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
QQY     122 VQDWVAYLETRLADWIHSSGCGWASFTALYG 152
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Ddb     122 IAAWMATYLNRLEPWIQENGWDTFVELYG 152
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RESULT 12
US-10-277-693A-10
; Sequence 10, Application US/10277693A
; Publication No. US20030096367A1
; GENERAL INFORMATION:
; APPLICANT: Korsmeyer, Stanley J.
; TITLE OF INVENTION: Cell Death Agonists
; FILE REFERENCE: 56029/36280
; CURRENT APPLICATION NUMBER: US/10/277,693A
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/379,820
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 08/112,208
; PRIOR FILING DATE: 1993-08-26
; PRIOR APPLICATION NUMBER: 08/856,034
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-277-693A-10

Query Match      40.5%; Score 408.5; DB 15; Length 239;
Best Local Similarity 36.6%; Pred. No. 4.2e-36;
Matches 86; Conservative 35; Mismatches 59; Indels 55; Gaps 5;

QQY      9 DTRALVAQFVGVRQRKGVCVCGAG-----PGE----- 35
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Ddb     10 DNREIVMKIHYKLSRGVDEWDAGVGAAPPGAAPAGPIFSQPGHTPHFAASRDPPVART 69
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
QQY      36 -----GRAADP-----LHQAMEAAGDEETFRFTSFDAQLHVTPGSAQQR 78
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Ddb     70 SFLOTPAAPAAGAAGPALSPVPVWHUTLRQAGDDFSRRYRDDFAEMSSQLHLTPPTARGR 129
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
QQY      79 FTQVSDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQVQDWVAVLETRLADWI 138
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Ddb     130 FATVVELFRDGVNWGRIVAFVFEFGVGVCSVNREMSPLDVNDIALHWTEYLNRHLHTWI 189
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
QQY     139 HSSGCGWAFTALYGDGALEEARLEREGNWSVRTLTGVALGALVTVGAFPAFK 193
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Ddb     190 QDNGGWDAFVELYG---PSMRPLDFSWLSLKTLTLLSAL-VGCITILGAILGHX 239
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

RESULT 13
US-08-726-211-5
; Sequence 5, Application US/08726211
; Publication No. US20030012812A1
; GENERAL INFORMATION:
; APPLICANT: Tormo, Mar
; APPLICANT: Tari, Ana M.
; APPLICANT: Lopez-Berestein, Gabriel
; TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY
; TITLE OF INVENTION: LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
```

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STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/726,211
  FILING DATE: Concurrently Herewith
  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
  NAME: Wilson, Mark B.
  REGISTRATION NUMBER: 37,259
  REFERENCE/DOCKET NUMBER: JTXC:504
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (512) 418-3000
  TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 239 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
    MOLECULE TYPE: protein
US-08-726-211-5

Query Match      40.3%; Score 406.5; DB 8; Length 239;
Best Local Similarity 36.6%; Pred. No. 7e-36;
Matches 86; Conservative 36; Mismatches 58; Indels 55; Gaps 5;

QY 9 DTRALVADFVGYRLRQKGYVCGAG-----PGE----- 35
DB 10 DNRREIVMKYIHYKLSQRYEWDAAGVGAAPGAPGIFSSQPGHTPHPAASRDVPART 69
QY 36 -----GPAADP-----LHQAMRAAGDEPETFRFRFSDLAACLHVTPGSAQOR 78
DB 70 SPLQTPAAPGAAAGPALSPPVPPVHLALRQAGDDFSRRYRGDFAEKSSQLHLPFTARGR 129
QY 79 FTQVSDLELFGQGNWGRVAVFFVFGAALCAESVNKEMEPLVGVQVQDMWVAYLETRLADWI 138
DB 130 FATVVEELFRDGVNMGRIVAFFFGVGVNREMSPLVDNIALMWTYLNRRHLHTWI 189
QY 139 HSSGGWAEFTALYGDGALAEARLRREGNWNASVRTVLTGAVALGALVTVGAFPAASK 193
DB 190 QDNGGWDAFVELYG----PSMRPLDFSWLSKLTLLSLAL-VGACITLGLAYLSHK 239

RESULT 15
US-10-053-645A-21
; Sequence 21, Application US/10053645A
; Publication No. US20030176376A1
; GENERAL INFORMATION:
; APPLICANT: Robert E. Klem
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
; TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
; TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
; FILE REFERENCE: 10412-022-999
; CURRENT APPLICATION NUMBER: US/10/053,645A
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,244
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-053-645A-21

Query Match      40.3%; Score 406.5; DB 12; Length 239;
Best Local Similarity 36.6%; Pred. No. 7e-36;
Matches 86; Conservative 36; Mismatches 58; Indels 55; Gaps 5;

QY 9 DTRALVADFVGYRLRQKGYVCGAG-----PGE----- 35
DB 10 DNRREIVMKYIHYKLSQRYEWDAAGVGAAPGAPGIFSSQPGHTPHPAASRDVPART 69
QY 36 -----GPAADP-----LHQAMRAAGDEPETFRFRFSDLAACLHVTPGSAQOR 78
DB 70 SPLQTPAAPGAAAGPALSPPVPPVHLALRQAGDDFSRRYRGDFAEKSSQLHLPFTARGR 129
QY 79 FTQVSDLELFGQGNWGRVAVFFVFGAALCAESVNKEMEPLVGVQVQDMWVAYLETRLADWI 138
DB 130 FATVVEELFRDGVNMGRIVAFFFGVGVNREMSPLVDNIALMWTYLNRRHLHTWI 189
QY 139 HSSGGWAEFTALYGDGALAEARLRREGNWNASVRTVLTGAVALGALVTVGAFPAASK 193
DB 190 QDNGGWDAFVELYG----PSMRPLDFSWLSKLTLLSLAL-VGACITLGLAYLSHK 239

Search completed: October 24, 2003, 11:04:41
Job time : 46.5 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 24, 2003, 10:44:00 ; Search time 25 Seconds
(without alignments)
742.422 Million cell updates/sec

Title: US-09-925-674A-9
Perfect score: 1009
Sequence: 1 MATFASPTDPTRALVADFGV.....LTGVALGALVTGGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*

1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	425.5	42.2	233	2 I49056	bcl-x long - mouse
2	424.5	42.1	233	2 B47537	apoptosis regulator
3	421.5	41.8	233	2 S51761	BCL-X protein - ra
4	420.5	41.7	233	2 A37332	transforming prote
5	411	40.7	232	2 S24390	transforming prote
6	408.5	40.5	239	1 TVHUA1	transforming prote
7	408	40.4	236	2 I67432	BCL-2 - rat fragm
8	403	39.9	236	2 I53744	Gene bcl-2 protein
9	402	39.8	236	1 TVMSA1	transforming prote
10	401.5	39.8	233	2 I67431	BCL-X-long - rat
11	399	39.5	236	2 JC7383	B-cell lymphoma 2
12	375	37.2	190	2 A47537	apoptosis regulator
13	374.5	37.1	214	2 I49057	bcl-x transmembran
14	371.5	36.8	227	2 JE0203	apoptosis regulator
15	353	35.0	216	2 B37332	transforming prote
16	345.5	34.2	199	1 TVMSB1	transforming prote
17	342	33.9	205	1 TVHUB1	transforming prote
18	277.5	27.5	154	2 I58194	gene bcl-2 protein
19	179	17.7	170	2 I49055	bcl-x short - mous
20	174	17.2	211	2 S58873	Bak protein - huma
21	171	16.9	176	2 I67435	gene bcl-xshort pr
22	169	16.7	211	2 S58875	cdn-2 protein - hu
23	158.5	15.7	192	2 D47538	bcl-2-associated p
24	154	15.3	192	2 A47538	bcl-2-associated p
25	154	15.3	261	2 H88578	protein ced-9 [imp
26	154	15.3	280	2 A53289	apoptosis suppress
27	150.5	14.9	133	2 I53295	bcl-2-associated p
28	147.5	14.6	179	2 JC7355	Bax-delta protein
29	147.5	14.6	218	2 B47538	bcl-2-associated p

ALIGNMENTS

RESULT 1
I49056
bcl-x long - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I49056; S52866
R:Farq. W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A:Reference number: I49055; MUID:95052604; PMID:7963517
A:Accession: I49056
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-233 <RES>
A:Cross-references: EMBL:U10101; NID:G506647; PIDN:AAA82173.1; P.D:G506648
R:Xamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
submitted to the EMBL Data Library, November 1994
A:Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line thr
A:Reference number: S52866
A:Accession: S52866
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-233 <AM>
A:Cross-references: EMBL:X83574; NID:G695622; PIDN:CAA58557.1; PID:G695623
C:Superfamily: bcl transforming protein

Query Match 42.2% Score 425.5; DB 2; Length 233;
Best Local Similarity 40.9%; Pred. No. 4.2e-32;
Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 4;
QY 11 RALVADFVGYRLRQKY-----V 28
DB 6 RELVVDFLSYKLSQKGSWSQSFQVVEENRTEAPEAEETPSAINGPSWHLADSPAV 65
QY 29 CGAGGCEGPAAD-----PLHQAMRAAGDEFFTRFRRTTSDLAALHVTGPSAQCRPT 80
DB 66 NGA-TGHSSSDAREVTPMAAVKQALREAGDEFFRYRRAFSQSLQHLITPGYQSF 124
QY 81 QVSDDELFCGGNWRGLVAFVFFVFGAALCAESYKMEPLVGVQVQWVAYLETRLADWHS 140
DB 125 QVWNELFEDGVNWRGRIVAFPSFGGALCVESVDKEMQVLSRIASWMTYLNHLEPWIQE 184
QY 141 SGWAEFTALYGDGALFEARELRE--GNWASVRTVLFGAVALGAL 183
DB 185 NGGMDTFVDLYGNNAABSRKQERFNRFLTGMTVAGVLLGSL 229

RESULT 2
B47537
apoptosis regulator bcl-xL - human
N:Alternate names: bcl-2-related protein
N:Contains: apoptosis regulator bcl-xs

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C:Species: Homo sapiens (man)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C:Accession: B47537; C47537
R:Boise, L.H.; Gonzalez-Garcia, Y.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell74, 597-608, 1993
A:Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptosis
A:Reference number: A47537; MUID:93364977; PMID:8358759
A:Accession: B47537
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-233 <BOI>
A:Cross-references: GB:L20121; NID:G510900; PIDN:CAA80661.1; PID:G510901
A:Accession: C47537
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-69, 'G', 71-125, 189-233 <BO2>
A:Cross-references: GB:L20122; NID:G623236; PIDN:CAA80662.1; PID:G623237
C:Genetics:
A:Gene: GDB:BCL2L
A:Cross-references: GDB:228079
C:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; apoptosis
F:1-233/Product: apoptosis regulator bcl-xL #status predicted <MA2>
F:1-125,189-233/Product: apoptosis regulator bcl-XS #status predicted <MA2>
Query Match 42.1%; Score 424.5; DB 2; Length 233;
Best Local Similarity 40.2%; Pred. No. 5.2e-32;
Matches 90; Conservative 24; Mismatches 59; Indels 51; Gaps 4;
QY 1: RALVADFGVRLRQKGY-----PLHQAMRAAGDEFTFRPTFSDLAALQHLVTPGSAQORFTQ 39
DB 6 RELVDFLSYKLSQKGYSWQSFSDVENRTEAPEGTESEMETPSAINGNPSMHLADSPAV 65
QY 40 D-----LHQAMRAAGDEFTFRPTFSDLAALQHLVTPGSAQORFTQ 81
DB 66 NGATASSS:DAREVTPMAAVKQALREAGDEFELRYRAFSDLTQSJHTPGTAYQSFQ 125
QY 82 VSEDFQGGPNWGRVLAFFVFGAALCAESVNKEMEPLVGVQVQDMMVAYLETSLADWIHSS 141
DB 126 VNELFRDGVNMGRIVAFFSFGGALCVESVDKEMQVLSRIAAMWATYLNDRLEPWIOEN 185
QY 142 GWAETALYGDGALAEARLRE--GNWASVRTVLGTGAVLALGAL 183
DB 186 GGMDFVELYGNNAASRSKQGERFNRWFLTGMTVAGVVLLGSL 229
RESULT 3
BCL-X protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
C:Accession: S51761; S5-762
R:Michaelidis, T.M.
submitted to the EMBL Data Library, November 1994
A:Reference number: S51761
A:Accession: S51761
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <MIC>
A:Cross-references: EMBL:X82537; NID:G607176; PIDN:CAA57886.1; PID:G607177
A:Experimental source: embryonic; brain
A:Accession: S51762
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-125,189-233 <MI2>
A:Cross-references: EMBL:X82537; NID:G607176; PIDN:CAA57887.1; PID:G607178
A:Experimental source: embryonic; brain
A:Note: smaller form due to splicing
C:Genetics:
A:Introns: 125/3
C:Superfamily: bcl transforming protein
Query Match 41.8%; Score 421.5; DB 2; Length 233;
Best Local Similarity 40.8%; Pred. No. 9.8e-32;
Matches 91; Conservative 23; Mismatches 56; Indels 53; Gaps 4;
QY 13 LVADFGVRLRQKGY-----PLHQAMRAAGDEFTFRPTFSDLAALQHLVTPGSAQORFTQV 30
DB 8 LWDPLFSYKLSQKGYSWQSFSDVENRTEAPEGTESEMETPSAINGNPSMHLADSPAVNG 67
QY 31 AGPGECPAAD-----PLHQAMRAAGDEFTFRPTFSDLAALQHLVTPGSAQORFTQV 82
DB 68 A-TGHSSSLDAREVTPMAAVKQALREAGDEFELRYRAFSDLTQSJHTPGTAYQSFQV 126
QY 83 SDELFQGGPNWGRVLAFFVFGAALCAESVNKEMEPLVGVQVQDMMVAYLETSLADWIHSSG 142
DB 127 VNELFRDGVNMGRIVAFFSFGGALCVESVDKEMQVLSRIAAMWATYLNDRLEPWIOEN 186
QY 143 GWAETALYGDGALAEARLRE--GNWASVRTVLGTGAVLALGAL 183
DB 187 GMDTFVDLYGNNAASRSKQGERFNRWFLTGMTVAGVVLLGSL 229
RESULT 4
A37332
transforming protein (bcl-2-alpha) - chicken
C:Species: Gallus gallus (Chicken)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Feb-1997
C:Accession: A37332; S35453
R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a var
A:Reference number: A37332; MUID:92375724; PMID:1508712
A:Accession: A37332
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-233 <EGU>
A:Cross-references: EMBL:D11381
C:Genetics:
A:Introns: 189/3
C:Superfamily: bcl transforming protein
C:Keywords: mitochondrion; transforming protein; transmembrane protein
Query Match 41.7%; Score 420.5; DB 2; Length 233;
Best Local Similarity 37.6%; Pred. No. 3.2e-31;
Matches 86; Conservative 33; Mismatches 61; Indels 49; Gaps 4;
QY 9 DTRALVADFGVRLRQKGYCGAG-----PGGPAADP-----PGGPAADP----- 41
DB 10 DNREIVLVKYLKLSQKGYDWAAGDRPPVPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 69
QY 42 -----LHQAMRAAGDEFTFRPTFSDLAALQHLVTPGSAQORFTQVSD 84
DB 70 AASEVPPAEGLRPAPPVGHLLALRQAGDEFRRYQDRDFAQNSGQLHETFTAGRGFVAVVE 129
QY 65 ELFGGPNWGRVLAFFVFGAALCAESVNKEMEPLVGVQVQDMMVAYLETSLADWIHSSGW 144
DB 130 ELFRDGVNMGRIVAFFSFGGALCVESVNREMSPLVDNIATMTWTEYLNDRLEPWIOEN 189
QY 145 ABFTALYGDGALAEARLREGNWASVRTVLGTGAVLALGALVTVGAFFASK 193
DB 190 DAFVELYGN---SMRPLDFSWISLTKILS-LVLVGACITLGAVALGHK 233
RESULT 5
S24390
transforming protein (Bcl-2) homolog - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S24390
R:Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
Biochim. Biophys. Acta 1132, 109-113, 1992
A:Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homolog
A:Reference number: S24390; MUID:92379084; PMID:1511008
A:Accession: S24390
A:Status: preliminary
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A:Molecule type: mRNA
A:Residues: 1-232 <CAZ>
A:Cross-references: EMBL:Z1196.; NID:g62969; PIDN:CAA78018.1; PID:g62970
C:Superfamily: bcl transforming protein
C:Keywords: mitochondrion; transmembrane protein

Query Match 40.7%; Score 411.; DB 2; Length 232;
Best Local Similarity 37.3%; Pred. No. 9.2e-31; Mismatches 62; Indels 48; Gaps 4;
Matches 85; Conservative 33;

QY 9 DTRALVADFVGYRLRQKGYVCGAG-----PGSGPAADP----- 41
Db 10 DNREIVMKYIHYKLSQGYDWAAGEDRPVPAPAPAPAAVAAGACASHRPSPPAR. 69
QY 42 -----LHOAMRAAGDEFFETFRFTSDLAALQHLVTPGSAOORFTQVSDE 85
Db 70 LLVRCPLRGCAAPGGVHLALRQAGDFFSRYYORDFAQMSQQLHLPFTATGRFAVVEE 129
QY 86 LFOGSPNMGRLVAFVFGAALCAESVNKEMEPVGVQVQDMVMVAYLETRLADWIHSSGWA 145
Db 130 LFRDGVNWRIVAFEFPGVCMVESVNREKSPVDN:ATW:TEYLNKHLHNIQDNGKD 189
QY 146 EFTALYDGGALAEARRREGNWSVRTLTGAVALGALVTVGAPFASK 193
Db 190 AFVVELYGN----SKRPLDFDSWISLKLILS-LVLVGACITLGAYLGHK 232

RESULT 6
TVHUAL
transforming protein bcl-2, splice form alpha - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1998 #sequence revision 07-Jun-1996 #text_change 15-Oct-1999
C:Accession: C37332; A29409; S02452; A24428; A27622; B27622
R:Bguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues
A:Reference number: A37332; MUID:92375724; PMID:1506712
A:Accession: C37332
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-239 <EGU>
A:Note: this report is a correction
R:Tsujimoto, Y.; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene for the B-cell lymphoma
A:Reference number: A29409; MUID:86259760; PMID:3523487
A:Accession: A29409
A:Molecule type: mRNA
A:Residues: 1-95 'A', 97-109, 'G', 111-236, 'S', 238-239 <TSJ>
A:Cross-references: GB:M13994; NID:g179366; PIDN:AAA51813.1; PID:g179367
A:Note: this sequence has been corrected in reference A37332
R:Seo, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer, S.J.
EMBO J. 7, 123-131, 1988
A:Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2 gene in human B-cell lymphomas
A:Reference number: S02452; MUID:98196071; PMID:2834197
A:Accession: S02452
A:Molecule type: mRNA
A:Residues: 1-239 <SET>
R:Cleary, M.L.; Smith, S.D.; Sklar, J.
Cell 47, 19-28, 1986
A:Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin heavy chain enhancer
A:Reference number: A24428; MUID:87002468; PMID:2875799
A:Accession: A24428
A:Molecule type: mRNA
A:Residues: 1-58, 'T', 60-116, 'R', 118-239 <CLE>
A:Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371
R:Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakshi, A.
Oncogene Res. 2, 263-275, 1988
A:Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma: evidence for a bcl-2 gene
A:Reference number: A27622; MUID:98217344; PMID:3285301
A:Accession: A27622
A:Molecule type: mRNA
A:Residues: 1-58, 'T', 60-239 <HUA>
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A:Accession: B27622
A:Molecule type: DNA
A:Residues: 1-6, 'S', 8-58, 'T', 60-128, 'C', 130-239 <HJA2>
A:Note: the sequence was determined from the germline gene
C:Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation
C:Genetics:
A:Gene: GDB:BCL2
A:Cross-references: GDB:119031; OMIM:151430
A:Map position: 18q21.3-18q21.3
C:Function:
A:Description: blocks apoptosis in hematopoietic cells
C:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; pre-B-cell leukemia

Query Match 40.5%; Score 408.5; DB 1; Length 239;
Best Local Similarity 36.6%; Pred. No. 1.6e-30;
Matches 86; Conservative 35; Mismatches 59; Indels 55; Gaps 5;

QY 9 DTRALVADFVGYRLRQKGYVCGAG-----PGS----- 35
Db 10 DNREIVMKYIHYKLSQGYDWAAGDVGAAAPGAPGIFSSQPGHTPHPAASRDPVART 69
QY 36 -----GPAADP-----LHOAMRAAGDEFFETFRFTSDLAALQHLVTPGSAOOR 79
Db 70 SPLQTPAAGAAAGPALSPVPPVHLTLRQAGDDFSRYYRDRDFAEKSSQLH:TPFTARGR 129
QY 79 FTQVSDDELFOGSPNMGRLVAFVFGAALCAESVNKEMEPVGVQVQDMVMVAYLETRLADWI 138
Db 130 FATVVEELFRDGVNWRIVAFEFPGVCMVESVNREKSPVDN:ALWMTEY:LNRLHWTW: 189
QY 139 HSSGWAEBFTALYDGGALAEARRREGNWSVRTLTGAVALGALVTVGAPFASK 193
Db 190 QNCGWDAPVELYG----PSMRPLDFDSWISLKLILS-LVLVGACITLGAYLGHK 239

RESULT 7
BCL-2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I67432
R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equi-
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A:Reference number: I53295; MUID:95129487; PMID:7828536
A:Accession: I67432
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-236 <RES>
A:Cross-references: EMBL:U34964; NID:g1004378; PIDN:AAA77687.1; PID:g1004379
C:Superfamily: bcl transforming protein

Query Match 40.4%; Score 408; DB 2; Length 236;
Best Local Similarity 35.8%; Pred. No. 1.8e-30;
Matches 83; Conservative 35; Mismatches 62; Indels 52; Gaps 3;

QY 9 DTRALVADFVGYRLRQKGY----- 27
Db 10 DNREIVMKYIHYKLSQGYDWDGDSAPLRRAPTGPFGFSQPESNRTPAVHRDTAART 69
QY 28 -----VCGAGGCGPAADPLHOAMRAAGDEFFETFRFTSDLAALQHLVTPGSAOORFTQ 81
Db 70 SPLRLVANAGPALSPPVPPVHLTLRRAGDDFSRYYRDRDFAEKSSQLH:TPFTARGREAT 129
QY 82 VSDLELFOGSPNMGRLVAFVFGAALCAESVNKEMEPVGVQVQDMVMVAYLETRLADWIHSS 141
Db 130 VVEELFRDGVNWRIVAFEFPGVCMVESVNREKSPVDN:ALWMTEY:LNRLHWTW: 189
QY 142 GWAEBFTALYDGGALAEARRREGNWSVRTLTGAVALGALVTVGAPFASK 193
Db 190 GCMWDAPVELYG----PSMRPLDFDSWISLKLILS-LVLVGACITLGAYLGHK 236
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RESULT 8
153744
gene bcl-2 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C:Accession: I53744
R:Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
Gene 140, 291-292, 1994
A:Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.
A:Reference number: I53744; MUID:94193015; PMID:814404
A:Accession: I53744
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-236 <RES>
A:Cross-references: GB:L14680; NID:9408946; PIDN:AAA53662.1; PID:9408947
C:Genetics:
A:Gene: bcl-2
C:Superfamily: bcl transforming protein

Query Match 39.9%; Score 403; DB 2; Length 236;
Best Local Similarity 35.3%; Pred. No. 5.2e-30; Mismatches 63; Indels 52; Gaps 3;
Matches 82; Conservative 35;

QY 9 DTRALVADFGVYRLRQKGYCGAG-----PG----- 34
DB 10 DNREIVMKYIHYKLSQRCYEWDAAGDADAAPLGAFAFTPGIISFQFQSPNPMFAVHREXAART 69

QY 35 -----EGPAADP-----LHQAMRAAGDEFTFRFRFTSDLAALQHLVTPGSAQORFTQ 81
DB 70 SPLRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRDRFAEMSSQLHLTPFTARGRFAT 129

QY 82 VSDELFCGGPNWGRVLAFFVFGAALCAESVNKEPELVGVQVQDMVAYLETRLADWIHSS 141
DB 130 VVEELFRDGVNMGRIVAFFEFEGVMCVSNRENSPLVDNIALMMTEYLNRHLHTWIQDN 189

QY 142 GWAEEFTALYGDGALEEARLRREGNMAASVRTLTGAVAGALVTVGAFFASK 193
DB 190 GWDADFVELYG-----PSMRPLDFSWLSLKLTLSS-LPWGACITLGGAYLGHK 236

RESULT 10
167431
BCL-X-Long - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I67431
R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equi-
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A:Reference number: I53295; MUID:95129487; PMID:7828536
A:Accession: I67431
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-233 <RES>
A:Cross-references: EMBL:U34963; NID:g1004376; PIDN:AAA77686.1; PID:g1004377
C:Superfamily: bcl transforming protein

Query Match 39.8%; Score 401.5; DB 2; Length 233;
Best Local Similarity 39.1%; Pred. No. 7.1e-30;
Matches 88; Conservative 23; Mismatches 61; Indels 53; Gaps 4;

QY 11 RALVADFGVYRLRQKGY-----V 28
DB 6 RELVVDFLSYKLSQKGYSWQSOPDVENRTEAPETPEPTPSAINGNFSWHLADSPAV 65

QY 29 CGAGPGEPAAD-----PLHQAMRAAGDEFTFRFRFTSDLAALQHLVTPGSAQORFT 80
DB 66 NGA-TGHSSSLDAREVLPAAVKQALREAGDEFFELRYRRAFSDLTSQLHTPGTVYQSFE 124

QY 81 QVSEDLFCGGPNWGRVLAFFVFGAALCAESVNKEPELVGVQVQDMVAYLETRLADWIHSS 140
DB 125 QVNEELFRDGVNMGRIVAFFEFEGVMCVSNRENSPLVDNIALMMTEYLNRHLHTWIQDN 184

QY 141 SGWAEFTALYGDGALEEARLRREGNMAASVRTLTGAVAGALVTVGAFFASK 183
DB 185 NGGMDTFVDLYGNNTAPESRKQGERFRNRFVLTGMTVAGVVLGSL 229

RESULT 11
JC7383
B-cell lymphoma 2 protein - Chinese hamster
C:Species: Crictetus griseus (Chinese hamster)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 08-Dec-2000
C:Accession: JC7383
R:Tomicic, M.T.; Christmann, M.; Kaina, B.
Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A:Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A:Reference number: JC7383
A:Accession: JC7383
A:Contents: Ovary
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-236 <TOM>
A:Cross-references: GB:AJ271720
C:Comment: This protein has anti-apoptotic function, and supports cell survival.
C:Genetics:

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A:Gene: bcl-2
C:Superfamily: bcl transforming protein
C:Keywords: B-cell lymphoma; ovary

Query Match 39.5%; Score 399; DB 2; Length 236;
Best Local Similarity 34.9%; Pred. No. 1.2e-29;
Matches 81; Conservative 35; Mismatches 54; Indels 52; Gaps 3;

QY 9 DTRALVADFVGYRLRQKGY----- 27

DB 10 DNREIVMKYIHYKLSQRYEWDVDAAPLGAAPTFCIFSFQESNPTZAVHRDMAAT 69

QY 28 -----VCGAGPGSGPAADPLHQAYRAGDEFETRFRFTSDLAALQHLVTPGSAQQRFTQ 81

DB 70 SPLRPIVATCTGPTTSPVPVVLTLRAGDDFSRRYRCFAEMSSQLHLFTFTARGHAT 129

QY 82 VSDSEJFQGGPNWGRVLAFFVFGAALCAESVNKEMEPVGVQVQDMVYVLETRLDADW:HSS 141

DB 130 VVEELFRDGVNMGRIVAFFVFGVYVYVNSRENSPLVDNIALWNTEYLNPHLHTW:ICDN 193

QY 142 GGNWAEFTALYCGGALEEARLRREGNWSVRTVLTGVALGALVTVGAPFASK 193

DB 190 GGMADFVELYG----PSVRPLDFSMLSLTKLLSLAL-VGACITLGYLGHK 236

RESULT 12

A47537
A:Title: apoptosis regulator bcl-x - chicken
C:Species: Gallus gallus (Chicken)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C:Accession: A47537
R:Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turk, J.A.;
Cell 74, 597-608, 1993
A:Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A:Reference number: A47537; MUID:93364977; PMID:8358789
A:Accession: A47537
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-190 <BOI>
A:Cross-references: GB:223110; GB:L20120; NID:G510898; PIDN:CAA80657.1; PID:G510593
C:Superfamily: bcl transforming protein

Query Match 37.2%; Score 375; DB 2; Length 190;
Best Local Similarity 43.2%; Pred. No. 1.6e-27;
Matches 80; Conservative 15; Mismatches 44; Indels 46; Gaps 3;

QY 11 RALVADFVGYRLRQKGY-----VCGAGPGGEP----- 37

DB 6 RELVIDFVSKLSQRGHCWSLEEDENRTDAAEAEMDSVLNGSPSHPPAGHVNGAT 65

QY 38 -----AADPLHQAMRAAGDEFETRFRFTSDLAALQHLVTPGSAQQRFTQVSDE 85

DB 66 VHRSSLEVHEIVRASDVQRALRDAGDBFELRYRRAFSDLTSQLHTFTCTAYQSFQVNE 125

QY 86 LFQGGPNWGRVLAFFVFGAALCAESVNKEMEPVGVQVQDMVYVLETRLDADW:HSSGGWA 145

DB 126 LFRDGVNMGRIVAFFVFGALCVESVDKEMRLVGR:VSNMNTLTLDHLDPLQWQNGGW 185

QY 146 EFTAL 150

DB 186 R-TAL 189

RESULT 13

I49057
A:Title: bcl-x transmembrane deleted - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I49057
R:Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A:Reference number: I49055; MUID:95052604; PMID:7963517

A:Accession: I49057

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-214 <RES>

A:Cross-references: EMBL:U10102; NID:G506649; PIDN:AAA82174.1; PID:G506650

C:Genetics:

A:Gene: bcl-x-long

C:Superfamily: bcl transforming protein

Query Match 37.1%; Score 374.5; DB 2; Length 214;
Best Local Similarity 42.2%; Pred. No. 2.1e-27;
Matches 79; Conservative 17; Mismatches 40; Indels 51; Gaps 3;

QY 11 RALVADFVGYRLRQKGY-----V 28

DB 6 RELVDVFLSKLSQKGYSWQSQFSDVEENRTEAPEETEAEETPSAINGNPSWHLADSPAV 65

QY 29 CGAGPGGEPAA-----PLHQAMRAAGDEFETRFRFTSDLAALQHLVTPGSAQQRFT 80

DB 66 NGA-TGHSSSLDAREVIPAAYKQALREAGDEFELRYRRAFSDLTSQLHTFTCTAYQSF 124

QY 81 QVSDSEJFQGGPNWGRVLAFFVFGAALCAESVNKEMEPVGVQVQDMVYVLETRLDADW:HS 140

DB 125 QVYNELFRDGVNMGRIVAFFVFGALCVESVDKEMQVLVSRIASMWTYLNHLEPWIDE 184

QY 141 SGWAEFTALY 147

DB 185 NGGWDTF 191

RESULT 14

JE0203
A:Title: apoptosis regulator bcl-x isoform - human
N:Alternate names: h-bcl-xbeta
C:Species: Homo sapiens (man)
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 16-Jul-1999
C:Accession: JE0203
R:Han, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Techachler, E.
Biochem. Biophys. Res. Commun. 248, 147-152, 1998
A:Title: Identification of a human cDNA encoding a novel bcl-x isoform.
A:Reference number: JE0203; MUID:98340865; PMID:9675101
A:Accession: JE0203
A:Molecule type: mRNA
A:Residues: 1-227 <BAN>
A:Cross-references: GB:U72398; NID:G1622940; PIDN:AAB17354.1; PID:G1622941
C:Genetics:

A:Gene: bcl-x

A:Xap position: 20

C:Superfamily: bcl transforming protein

Query Match 36.8%; Score 371.5; DB 2; Length 227;
Best Local Similarity 40.3%; Pred. No. 4.2e-27;
Matches 81; Conservative 19; Mismatches 50; Indels 51; Gaps 3;

QY 11 RALVADFVGYRLRQKGY-----V 28

DB 6 RELVDVFLSKLSQKGYSWQSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

QY 29 CGAGPGGEPAA-----PLHQAMRAAGDEFETRFRFTSDLAALQHLVTPGSAQQRFT 80

DB 66 NGA-TGHSSSLDAREVIPAAYKQALREAGDEFELRYRRAFSDLTSQLHTFTCTAYQSF 124

QY 81 QVSDSEJFQGGPNWGRVLAFFVFGAALCAESVNKEMEPVGVQVQDMVYVLETRLDADW:HS 140

DB 125 QVYNELFRDGVNMGRIVAFFVFGALCVESVDKEMQVLVSRIAAMWTYLNHLEPWIDE 184

QY 141 SGWAEFTALYGDGALEEAR 161

DB 185 NGGWRTKPLVCPFLASQQR 205

RESULT 15

B37332

transforming protein (bcl-2-beta) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 24-Apr-1998
C:Accession: B37332; S35452
R:Eguchi, Y.; Ewert, D.J.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues
A:Reference number: A37332; MUID:92375724; PMID:1508712
A:Accession: B37332
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-216 <EGU>
A:Cross-references: EMBL:D11381; EMBL:D11382
C:Superfamily: bcl transforming protein

Query Match 35.0%; Score 353; DB 2; Length 216;
Best Local Similarity 37.8%; Pred. No. 2.1e-25;
Matches 70; Conservative 22; Mismatches 49; Indels 44; Gaps 2;

QY 9 DTRALVADFVGVRRLQKGYVCGAG-----PGEPPAADP----- 41
DB 10 DNRDIVLKYIHYKLSQRYDWAAGEDRPVPPAPAPAAVAAGASSHRRPEPPGSA 69
QY 42 -----LHQMRAAGDEFETFRRTFSDLAALHVTTPGSAQORFTQVSD 84
DB 70 AASEVPPPAEGLRPAPPGVHLALRQAGDEFERRRYQDFQMSGQLHLPFTAHRGRFVAVE 129
QY 85 ELFGGPNWGRVAFVFFVGRALCAESYNKEMEPVAVGOVDMWVAYLETRLADWTHSSGGW 144
DB 130 ELFRDGVNWRIVAFVFFVGRVNCVESVNRMSPLVDNIATWTBYLNRLHNLNWIQXGGW 189
QY 145 AEFTA 149
DB 190 VRACA 194

Search completed: October 24, 2003, 10:52:03
Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 24, 2003, 10:26:35 ; Search time 13.5 Seconds
(without alignments)
672.308 Million cell updates/sec

Title: US-09-925-674A-9

Perfect score: 1009

Sequence: 1 MATTPASTPDTFALVADFVGV.....LTGAVALGALVTYVGAPPASK 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1006	99.7	193	1 BCLW_MOUSE	P70345 mus musculus
2	997	98.8	193	1 BCLW_HUMAN	Q92843 homo sapien
3	647.5	64.2	228	1 ARL_XENLA	Q92843 xenopus lae
4	429.5	42.6	229	1 BCLX_CHICK	Q07816 gallus galli
5	428.5	42.5	233	1 BCLX_PIG	Q07737 sus scrofa
6	425.5	42.2	233	1 BCLX_MOUSE	Q64373 mus musculus
7	425.5	42.2	233	1 BCLX_RAT	P53563 rattus norv
8	424.5	42.1	233	1 BCLX_HUMAN	Q07817 homo sapien
9	420.5	41.7	233	1 BCL2_CHICK	Q00709 gallus galli
10	412.5	40.9	229	1 BCL2_BOVIN	Q02718 bos taurus
11	410	40.6	236	1 BCL2_RAT	P49950 rattus norv
12	409	40.5	236	1 BCL2_MOUSE	P10417 mus musculus
13	408.5	40.5	239	1 BCL2_HUMAN	P10415 homo sapien
14	399	39.5	236	1 BCL2_CRITIO	Q91458 cricetus
15	366	36.3	204	1 ARL_XENLA	Q91828 xenopus lae
16	175.5	17.4	208	1 BAK_MOUSE	Q08734 mus musculus
17	174	17.2	211	1 BAK_HUMAN	Q16611 homo sapien
18	169	16.7	211	1 BAK2_HUMAN	Q16611 homo sapien
19	156.5	15.5	192	1 BAXA_MOUSE	Q16611 homo sapien
20	155.5	15.4	192	1 BAXA_RAT	Q16611 homo sapien
21	154	15.3	192	1 BAXA_HUMAN	Q16611 homo sapien
22	154	15.3	280	1 CED9_CAEEL	P41958 caenorhabdi
23	148	14.7	192	1 BAXA_BOVIN	Q02703 bos taurus
24	147.5	14.6	218	1 BAXB_HUMAN	Q07814 homo sapien
25	144	14.3	177	1 NR13_COTJA	Q90343 coturnix cc
26	140.5	13.9	271	1 CSDF_CAEER	P41957 caenorhabdi
27	138.5	13.7	143	1 BAXD_HUMAN	P55269 homo sapien
28	119	11.8	175	1 BFL1_HUMAN	Q16548 homo sapien
29	116	11.5	350	1 MCL1_HUMAN	Q37820 homo sapien
30	115	11.4	194	1 BCLB_HUMAN	Q9hd36 homo sapien
31	105	10.4	172	1 BFL1_MOUSE	Q07440 mus musculus
32	99.5	9.9	179	1 EAR_ASFB2	Q07819 african swi
33	98.5	9.8	179	1 EAR_ASFB7	P42485 african swi

RESULT 1

ID	BCLW_MOUSE	STANDARD	PRT	193 AA
AC	P70345			
DI	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Apoptosis regulator Bcl-W (BCL2-like 2 protein).			
GN	BCL2L2 OR BCLW.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	(1)_TaxID=10090;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96358615; PubMed=8761287;			
RA	Gibson D., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,			
RA	Jenkins N.A., Sutherland G.R., Baker E., Adams C.M., Cory S.			
RT	"bcl-w", a novel member of the bcl-2 family, promotes cell survival.;			
RL	Oncogene 13:665-675(1996);			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/10J;			
RX	MEDLINE=98160183; PubMed=9500547;			
RA	Ross A.J., Wayne K.G., Moss J.E., Parlow A.F., Skinner M.K.,			
RA	Russell L.D., Macgregor G.R.;			
RT	"Testicular degeneration in Bclw-deficient mice.;"			
RJ	Nat. Genet. 18:251-256(1998).			
CC	-!- FUNCTION: PROMOTES CELL SURVIVAL.			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND			
CC	IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,			
CC	AND SALIVARY GLAND.			
CC	-!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC			
CC	FUNCTION.			
CC	-!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.			
CC	-!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.			
CC	-!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.			
CC	-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL: U59746; AAB09056.1; -			
DR	EMBL: AF030769; AAB86430.1; -			
DR	SSSP: Q07817; 1MAZ			
DR	MG: 168052; BCL2L2.			
DR	InterPro: IPR000712; BCL2_BH.			
DR	InterPro: IPR003093; BCL2_BH4.			
DR	InterPro: IPR002475; BCL2_family.			
DR	Pfam: PF0452; Bcl-2; 1.			

ALIGNMENTS

34	98.5	3.8	179	1	EAR_ASFB4	Q07818 african swi
35	87.5	8.7	660	1	SHC_BRAJA	P54924 bradyrhizob
36	86.5	8.6	3433	1	POIG_KUNJM	P14335 x genome po
37	86	8.5	275	1	DAPB_AGRTS	Q831v8 agrobacteri
38	84.5	8.4	358	1	GLNA_LACSA	P23712 lactuca sat
39	83.5	8.3	872	1	SYA_STRPN	Q97q48 streptococc
40	82.5	8.2	3430	1	POLG_WNV	P06935 w genome po
41	81.5	8.1	887	1	A4_DROME	P14599 drosophila
42	80.5	8.0	236	1	YJ94_ARCFU	O28285 archaeoglob
43	79	7.8	396	1	PORA_PYRFU	Q51804 pyrococcus
44	79	7.8	454	1	YB48_MYCTU	O06548 mycobacteri
45	79	7.8	454	1	YJ45_MYCTU	P95269 mycobacteri

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Db 61 FSDLAQLHVTGPSAQORFTQVSDLFQGGPNWGRJVAFFVFGAALCAESVKNEMEPLVG 120
QY 121 QVQWYAYLETRLADWHSXGNAETALYDGALEBARLRGNWASVRLTGTGVAL 160
Db 121 QVQWYAYLETRLADWHSXGNAETALYDGALEBARLRGNWASVRLTGTGVAL 160
QY 181 GALVTGGAFFASK 193
Db 181 GALVTGGAFFASK 193

RESULT 3
ARI_XENLA
ID ARI_XENLA STANDARD; PRC; 228 AA.
AC Q91827;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Apoptosis regulator R1 (XRI) (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
CX NCB1_TaxID=8355;
RN [1]
R2 SEQUENCE FROM N.A.
R3 TISSUE=Head;
R4 MEDLINE=95331613; PubMed=7607538;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
cell-survival genes.";
RL Gene 158:171-179 (1995).
CC -!- FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.
CC -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -!- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC BRAIN OF MID-METAMORPHIC TO POST-METAMORPHIC TADPOLES AND
CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X82462; CRA57845.1; -
DR HSP; Q07817; IMAZ.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SMO0285; BH4; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS00662; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane.
FT NON_TER 1
FT DOMAIN 120 139 BH1.
FT DOMAIN 171 186 BH2.
FT TRANSMEM 207 227 POTENTIAL.
SQ SEQUENCE 228 AA; 25068 MW; C499D449A585F8A9 CRC64;

Query March 64.2%; Score 647.5; DB 1; Length 228;
Best Local Similarity 67.9%; Pred. No. 6,1e-51;
Matches 125; Conservative 21; Mismatches 35; Indels 3; Gaps 1;

QY 10 TRALVADVGVRLKQGVCGGPGEGPAADPLHQCAMRAAGDEFTFRFTSDLAQLH 69

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Db 48 SRALVEDLVRYLKCQSLV---PEPSGAASCALHSMRAAGDEFEERFQAISEISTQIH 104
QY 70 VTPGSAQORFTQVSDLFQGGPNWGRJVAFFVFGAALCAESVKNEMEPLVGQVQWYAY 129
Db 105 VTPGTAYARFAEAVAGSLFQGGVNWGRJVAFFVFGAALCAESVKNEMSPLLPRIDMMVTY 164
QY 130 LETRLADWHSXGNAETALYDGALEBARLRGNWASVRLTGTGVALGALVTGAF 189
Db 165 LETRLADWHSXGNAETALYDGALEBARLRGNWASVRLTGTGVALGALVTGAF 224
QY 190 FASK 193
Db 225 FASK 228

RESULT 4
BCLX_CHICK
ID BCLX_CHICK STANDARD; PRC; 229 AA.
AC Q07816; Q98908;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-X (BCL2-like 1 protein).
GN BCL2L1 OR BCLX OR BCL-X.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
OC Gallus.
CX NCB1_TaxID=9031;
RN [1]
R2 SEQUENCE FROM N.A. (ISOFORM SHORT).
R3 MEDLINE=93364977; PubMed=8358789;
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Bing L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
of apoptotic cell death.";
RL Cell 74:597-608 (1993).
RN [2]
R2 SEQUENCE FROM N.A. (ISOFORM LONG).
R3 STRAIN=Hubbard White Mountain; TISSUE=Testis;
RX MEDLINE=97264485; PubMed=9110311;
RA Vilagrasa X., Mezquita C., Mezquita J.;
RT "Differential expression of bcl-2 and bcl-x during chicken
spermatogenesis.";
RL Mol. Reprod. Dev. 47:26-29 (1997).
CC -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
CC ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC ENVELOPE (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS:
CC Name=Long;
CC IsoId=Q07816-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q07816-2; Sequence=VSP_000514;
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYNPHOID
CC DEVELOPMENT.
CC -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC APOPTOTIC ACTIVITY (BY SIMILARITY).
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
CC EMBL; Z21110; CA80657.1; -.
CC PIR; A47537; A47537.
CC HSP; P53563; 1AF3.
CC InterPro; IPR000712; Bcl2 BH.
CC InterPro; IPR003093; Bcl2 BH4.
CC InterPro; IPR002475; BCL2 family.
CC InterPro; IPR004725; Bcl2_reg.
CC Pfam; PF00452; Bcl-2; 1.
CC Pfam; PF02180; BH4; 1.
CC SMART; SM00337; BCL; 1.
CC SMART; SM00265; BH4; 1.
CC TIGRFAMs; TIGR00865; bcl-2; 1.
CC PROSITE; PS50062; BCL2_FAMILY; 1.
CC PROSITE; PS01080; BH1; 1.
CC PROSITE; PS01258; BH2; 1.
CC PROSITE; PS01259; BH3; 1.
CC PROSITE; PS01260; BH4; 1.
CC PROSITE; PS50063; BH4_2; 1.
CC Apoptosis; Transmembrane; Alternative splicing.
CC DOMAIN 4 24 BH4.
CC FT DOMAIN 82 96 BH3.
CC FT DOMAIN 125 144 BH1.
CC FT DOMAIN 176 191 BH2.
CC FT TRANSMEM 206 223
CC FT VARSPIC 185 229
CC ERFVLDLYGNNAALRLKQGFNFKNLLTGATVAGVLLGLSL
CC LSRK -> VRTAUP (in isoform Short).
CC /FTID=VSP_000514.
CC SEQUENCE 229 AA; 25733 MW; A97D3A4D04C0E9DA CRC64;

```

Query Match 42.6%; Score 429.5; DB 1; Length 229;

Best Local Similarity 41.2%; Pred. No. 2e-31; Mismatches 23; Indels 49; Gaps 4;

Matches 94; Conservative 23; Mismatches 62; Indels 49; Gaps 4;

11 RALVADVGVYLRQKGY-----VCGAGFGEGP-----37

6 RELVIDFVSYKLSGRGHCWSELEEDENRTDTAAEAEMDSVLNGSFWSHPPAGHVNGAT 65

38 -----AADPHQAMRAAGDEFFETFRPTFSGLAAQLHVTGSAQCFQTQUSDE 85

66 VRSSSEVHEIVRASDVQRLRDAGDEFFELRYRAFSGLTSSQHLTPGTAYQFEQVWNE 125

86 LFQGGPNWGLVAPFVFGAALCAESVKNKEPLVGQVQDMMWVAYLETRLADWTHSSGGWA 145

126 LFHDGVNNGRIVAFVFFSGGALCVESVDKXRVLVGRIVSWMTYLTCHLDPNTOENGWE 185

146 EPTALYGGGALAEARRUREGNWASVRTVLTGAVALGALVTVGAFVASK 193

186 RFVDLYGNNA---AAELRKQGETFNKWLTLTGATVAGVLL-LGSLLSRK 229

RESULT 5

ID BCLX_PIG

AC 07737;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Apoptosis regulator Bcl-X (BCL2-like 1 protein).

GN BCL2L1 OR BCL2L OR BCLX.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99171363; PubMed=20072723;

RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;

RT "Quantification of cardioprotective gene expression in porcine

RT short-term hibernating myocardium.";

RL J. Mol. Cell. Cardiol. 31:147-158(1999).

CC FUNCTION: Potent inhibitor of cell death. Isoform Bcl-x(L) anti-

CC apoptotic activity is inhibited by association with SIVA isoform

CC 1. Inhibits activation of caspases (By similarity). Appears to

CC regulate cell death by blocking the voltage-dependent anion

CC channel (VDAC) by binding to it and preventing the release of the

CC caspase activator, cytochrome c, from the mitochondrial membrane.

CC SJUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By

CC similarity). Heterodimerization with BAX does not seem to be

CC required for anti-apoptotic activity (By similarity). Isoform Bcl-

CC x(L) binds to SIVA isoform 1 (By similarity).

CC SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear

CC envelope (By similarity).

CC DOMAIN: The BH4 domain is required for anti-apoptotic activity.

CC The BH1 and BH2 domains are required for both heterodimerization

CC with other Bcl2 family members and for repression of cell death.

CC PTM: Proteolytically cleaved by caspases during apoptosis (By

CC similarity). The cleaved protein, lacking the BH4 domain, has pro-

CC apoptotic activity (By similarity).

CC SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

CC SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

CC SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

CC SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

CC BELONGS TO THE BCL-2 FAMILY.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; AJ001203; CAA04597.1; -

HSP; Q07817; 1MAZ.

InterPro; IPR000712; Bcl2 BH.

InterPro; IPR003093; Bcl2 BH4.

InterPro; IPR002475; BCL2 family.

InterPro; IPR004725; Bcl2_reg.

Pfam; PF00452; Bcl-2; 1.

Pfam; PF02180; BH4; 1.

SMART; SM00337; BCL; 1.

SMART; SM00265; BH4; 1.

TIGRFAMs; TIGR00865; bcl-2; 1.

PROSITE; PS50062; BCL2_FAMILY; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01258; BH2; 1.

PROSITE; PS01259; BH3; 1.

PROSITE; PS01260; BH4; 1; 1.

PROSITE; PS50063; BH4_2; 1.

KW Apoptosis; Mitochondrion; Transmembrane.

FT DOMAIN 4 24 BH4.

FT DOMAIN 86 100 BH3.

FT DOMAIN 129 148 BH1.

FT DOMAIN 180 195 BH2.

FT TRANSMEM 210 226 POTENTIAL.

SQ SEQUENCE 233 AA; 2606 MW; 185F6FA0441912B2 CRC64;

Query Match 42.5%; Score 428.5; DB 1; Length 233;

Best Local Similarity 41.3%; Pred. No. 2.5e-31;

Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

11 RALVADVGVYLRQKGY-----V 28

6 RELVVDFFSYKLSQKGYSWQFTDVEENRTAEPTGTESEAEPTSPAINGNPSHILADSAV 65

29 CCAGPGEPPAAD-----PLHQAMRAAGDEFFETFRPTFSGLAAQLHVTGSAQCFQT 80

66 NGA-TGHSSSLDAREVPMVAVKQALREAGDEFFELRYRAFSGLTSSQHLTPGTAYQSF 124

81 QVSDLFQGGPNWGLVAPFVFGAALCAESVKNKEPLVGQVQDMMWVAYLETRLADWTHS 140

125 QVNLFLFRDGVNNGRIVAFVFFSGGALCVESVDKXRVLVGRIVSWMTYLTCHLDPNTO 184

QY 141 SCQWAEFTALYGCALAEARRLR--GNWASVRTVLTCGVALGAL 183
 Db 185 NGGMDTFVELYGNNAAESRKQERNRWFMTGTMLAGVVLGSL 229

RESULT 6

BC1X_MOUSE STANDARD; PRT; 233 AA.
 AC Q64373; Q60657; Q60658; Q61338;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Apoptosis regulator Bcl-x (BCL2-like 1 protein).
 GN BC2L1 OR BCL2L OR BCLX.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2A4B;
 RA Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=9531139; PubMed=7607090;
 RA Gonzalez-Garcia M., Perez-Ballesteros R., Ding L., Duan L., Boise L.H.,
 RA Thompson C.B., Nunez G.;
 RT "Bcl-XL is the major bcl-x mRNA form expressed during murine
 development and its product localizes to mitochondria.";
 RL Development 120:3033-3042(1994).
 [3]
 RN SEQUENCE FROM N.A. (ISOFORMS X(L); X(S); AND X(Delta-TM)).
 RP TISSUE=Pre-B cell;
 RC MEDLINE=95052604; PubMed=7963517;
 RX Fang W., Rivard J.J., Mueller D.B., Behrens T.W.;
 RA "Cloning and molecular characterization of mouse bcl-x in B and T
 lymphocytes.";
 RT J. Immunol. 153:4388-4398(1994).
 [4]
 RN SEQUENCE FROM N.A. (ISOFORM X(BETA)).
 RP STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RX MEDLINE=98051053; PubMed=9390687;
 RA Yang X.-F., Weber G.F., Cantor H.;
 RT "A novel Bcl-x isoform connected to the T cell receptor regulates
 apoptosis in T cells.";
 RL Immunity 7:629-639(1997).
 [5]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97289584; PubMed=9144489;
 RX Gilliot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,
 RA Ohta S., Seldin M.F., Nunez G.;
 RT "Genomic organization, promoter region analysis, and chromosome
 localization of the mouse bcl-x gene.";
 RL J. Immunol. 158:4750-4757(1997).
 CC -!- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-x(L) anti-
 apoptotic activity is inhibited by association with SIVA isoform
 1. Inhibits activation of caspases (By similarity). Appears to
 regulate cell death by blocking the voltage-dependent anion
 channel (VDAC) by binding to it and preventing the release of the
 caspase activator, cytochrome c, from the mitochondrial membrane.
 CC The Bcl-x(S) isoform promotes apoptosis.
 CC -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
 similarity). Heterodimerization with BAX does not seem to be
 required for anti-apoptotic activity (By similarity). Isoform Bcl-
 x(L) binds to Siva isoform 1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
 envelope for Bcl-x(L). Cytoplasmic for Bcl-x(delta-TM).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=4;
 CC Name=BCX-X(L);

CC IsoId=Q64373-1; Sequence=Displayed;
 CC Name=BCL-X(S);
 CC IsoId=Q64373-2; Sequence=VSP_000517;
 CC Name=BCL-X(beta);
 CC IsoId=Q64373-3; Sequence=VSP_000518;
 CC Name=BCL-X(delta-TM);
 CC IsoId=Q64373-4; Sequence=VSP_000519;
 CC -!- TISSUE SPECIFICITY: Widely expressed, with highest levels in the
 brain, thymus, bone marrow, and kidney. Bcl-x(L) and Bcl-x(delta-
 TM) expression is enhanced in B and T lymphocytes that have been
 activated.
 CC -!- DEVELOPMENTAL STAGE: Bcl-x(beta) is expressed in both embryonal
 and postnatal tissues, whereas Bcl-x(L) is predominantly found in
 postnatal tissues.
 CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
 CC The BH1 and BH2 domains are required for both heterodimerization
 with other Bcl2 family members and for repression of cell death.
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis (By
 similarity). The cleaved protein, lacking the BH4 domain, has pro-
 apoptotic activity (By similarity).
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See http://www.isb-sib.ch/announce/
 or send an email to license@sib-sib.ch).
 CC
 CC EMBL: X81574; CAAS5557.1; -
 CC EMBL: L35049; AAS5039.1; -
 CC EMBL: L35048; AAS5040.1; -
 CC EMBL: U10102; AAB82174.1; -
 CC EMBL: U10101; AAB82173.1; -
 CC EMBL: U10100; AAB82172.1; -
 CC EMBL: U51279; AAC53463.1; -
 CC EMBL: U78031; AAB96881.1; -
 CC EMBL: U78030; AAB96881.1; JOINED.
 CC PIR: I49055; I49055.
 CC PIR: I49056; I49056.
 CC PIR: I49057; I49057.
 CC HSSP: P53563; IAF3.
 CC MGD: MGI:89139; Bcl2l.
 CC InterPro: IPR000712; Bcl2_BH.
 CC InterPro: IPR003093; Bcl2_BH4.
 CC InterPro: IPR002475; Bcl2_family.
 CC InterPro: IPR004725; Bcl2_reg.
 CC Pfam: PF00452; Bcl-2; 1.
 CC Pfam: PF02180; Bcl-2; 1.
 CC SMART: SM00337; BCL; 1.
 CC SMART: SM00265; BH4; 1.
 CC TIGRFAMs: TIGR00865; bcl-2; 1.
 CC PROSITE: PS00062; BCL2_FAMILY; 1.
 CC PROSITE: PS01080; BH1; 1.
 CC PROSITE: PS01258; BH2; 1.
 CC PROSITE: PS01258; BH3; 1.
 CC PROSITE: PS01259; BH3; 1.
 CC PROSITE: PS01260; BH4; 1.
 CC PROSITE: PS0063; BH4; 2; 1.
 CC Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
 CC DOMAIN 4 24 BH4.
 CC DOMAIN 86 100 BH3.
 CC DOMAIN 129 148 BH1.
 CC DOMAIN 180 195 BH2.
 CC TRANSMEM 210 226 POTENTIAL.
 CC VARSPPLIC 126 188 Missing (in isoform BCL-X(S)).
 CC FTID=VSP_000517.
 CC DTFDLYGNNAAESRKQERNRWFMTGTMVAGVVLGSL
 CC FSRK -> VRTTPLYCPPLACVSLCEHP (in isoform
 FT FT
 FT VARSPPLIC 189 233

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FT FT BCL-X(beta)).
FT FT /FTid=VSP_000518.
FT FT LYGNAAAEKRGKQERFRNFWLTGVTWAGVVLGSLFSRKR
FT FT -> GHDCGCGSAGLTQLQSEVTRH (in isoform
FT FT BCL-X(delta-TM)).
FT FT /FTid=VSP_000519.
SQ SEQUENCE 233 AA: 261-32 MW: 2452AC79687E072E CRC64;
Query Match 42.28; Score 425.5; DB 1; Length 233;
Best Local Similarity 40.98; Pred. No. 4.6e-31;
Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 4;
Qy 11 RALVADRVGVRLRQXV-----PLHQAQAAGDEETRRRTESDLAOLHVTGSAQCRFT 8C
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6 RELVVDLSYKLSCKGYSQSGFSDVEENRTPEAPEATEARETPTSAINGNPSWELADSPAV 65
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 29 CGAGPGGPGPAD-----PLHQAQAAGDEETRRRTESDLAOLHVTGSAQCRFT 8C
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66 NGA-TGHSLSLDAREVPMMAVKQLRAGDEFEFLRYRRAFSDLSQLHTPTGTAQSFE 124
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 81 QVSDLEFQGGPNWGLVAFVFGAALCAESVKNMEELVQGVQDMVYVLETTLADMHS 140
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 125 QVNVNELFRDGNWGRIVAFPSFGGALCVESVDKEMQVLVSRIASWMACTYLNDHLEPWIQE 164
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 141 SGWAEETALYDGALEEARLR--GNWASVRTVLTGVALGAL 183
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 185 NGGWDTEFDLYGNNAAEKRGKQERFRNFWLTGVTWAGVVLGSL 229
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
RESULT 7
BCLX_RAT STANDARD; PRT; 233 AA.
AC AC P53563; P70613; P70614; Q62678; Q62836; Q64087; Q64128;
DT 01-OCT-1996 (Rel. 34, Created)
DT DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Apoptosis regulator Bcl-x (BCL2-like 1 protein).
GN GN BCL2L1 OR BCL2L OR BCLX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC TISSUE=Brain;
RA Wesselingh S.L., David G.L., Choi S., Velluona M., Hardwick J.M.;
RN Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RC TISSUE=Thymus;
RA MEDLINE=96278736; PubMed=8662675;
RA Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S., Ohta S.;
RP "An additional form of rat Bcl-x, Bcl-xbeta, generated by an
RT unspliced RNA, promotes apoptosis in promyeloid cells.";
RL J. Biol. Chem. 271:13258-13265(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
RX MEDLINE=95129487; PubMed=7828536;
RA Tilly J.L., Tilly K.I., Kenton M.L., Conson A.L.;
RT "Expression of members of the bcl-2 gene family in the immature rat
RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT cell apoptosis is associated with decreased bax and constitutive
RT bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL Endocrinology 136:232-241(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=98010630; PubMed=9346936;
```

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DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1;
DR PROSITE; PS00063; BH4_2; 1.
KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
KW 3D-structure.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226
FT VARSPLIC 126 188
FT VARSPLIC 189 233
FT VARSPLIC 233
FT IDYSGD:PLGL (in isoform Bcl-X(S)).
FT FSRK -> VRTPLVPLVCLSSVEIPNCFPSPGKVVED
FT DTFVDLYGNNAASRKQERFNFILGTMTVAGVVLGSL
FT DTFVDLYGNNAASRKQERFNFILGTMTVAGVVLGSL
FT IDYSGD:PLGL (in isoform Bcl-X(beta)).
FT /FTid=VSP 000521.
FT R -> Q (IN REF. 1).
FT F -> S (IN REF. 2).
FT A -> E (IN REF. 2).
FT I -> L (IN REF. 4).
FT A -> V (IN REF. 4).
FT FF -> SS (IN REF. 4).
FT A -> T (IN REF. 4).
FT A -> P (IN REF. 4).
FT TURN 20 21
FT TURN 25 28
FT TURN 92 83
FT TURN 84 100
FT HELIX 106 112
FT TURN 116 117
FT HELIX 120 127
FT TURN 128 131
FT TURN 132 133
FT HELIX 137 156
FT TURN 157 158
FT TURN 160 161
FT HELIX 162 177
FT TURN 178 178
FT HELIX 179 184
FT TURN 185 186
FT HELIX 187 195
FT SEQUENCE 233 AA; 26158 MW; 2B62B6C63864BC8F CRC64;
Query Match 42.2%; Score 425.5; DB 1; Length 233;
Best Local Similarity 40.9%; Pred. No. 4.6e-31;
Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 4;
QY 11 RALVADFVGYLRQKGY-----V 28
DB 6 RELVVDFLSYKLSQKGYSGQSDVEENRTEAPEPEPTPSAINGPSWHLADSPAV 65
QY 29 CGAGGEGEPAAD-----PLHQNRAGDEFFETFRFTSDLAQHVTPGSAQORFT 80
DB 66 NGA-TGHSLSLDAREVIPMAAVKQALREAGDEFLRYRAFSDLTSQHIPTGTAYQSFE 124
QY 81 QVSDLEFQGGPNWGRIVAFVFGALCAESVKNKEPLVGVQDMMVAYLETRLDADHIS 140
DB 125 QVNVLEFRDGVNNGRIVAFVFFSGGALCVESVDKMQVLVSRIASNMATYLNHLEPIQE 184
QY 141 SGGWAEFTALYDGEALAEARLIRE--GNWASVRTVYTCGAVALGAL 183
DB 185 NGGMDTFVDLYGNNAASRKQERFNFILGTMTVAGVVLGSL 229
RESULT 8
BCLX_HUMAN STANDARD; PRT; 233 AA.
AC Q07817; Q92976;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Apoptosis regulator Bcl-X (BCL2-like 1 protein).
```

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GN BCL2L1 OR BCL2L OR BCLX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCB TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RX MEDLINE=93364977; PubMed=8358789;
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
RA "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT of apoptotic cell death.";
RL Cell 74:597-608(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM X(BETA)).
RA Inohara N., Ohta S.;
RA Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM X(L)).
RX TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Nadeau A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skaiska U., Smalhus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaiska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.
RX MEDLINE=95372373; PubMed=7644501;
RA Sedlak T.W., Oltvai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,
RA Korsmeyer S.J.;
RT "Multiple Bcl-2 family members demonstrate selective dimerizations
RT with Bax.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).
RN [5]
RP MUTAGENESIS OF BH1 AND BH2 DOMAINS.
RX MEDLINE=96170038; PubMed=8596636;
RA Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,
RA Korsmeyer S.J.;
RT "Bax-independent inhibition of apoptosis by Bcl-XL.";
RL Nature 379:554-556(1996).
RN [6]
RP INTERACTION WITH SIVA.
RX PubMed=12011449;
RA Xue L., Chu F., Cheng Y., Sur X., Borthakur A., Ramarao M., Pandey P.,
RA Wu M., Schlossman S.P., Prasad K.V.S.;
RT "Siva-1 binds to and inhibits BCL-X(L)-mediated protection against UV
RT radiation-induced apoptosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:6925-6930(2002).
RN [7]
RP STRUCTURE BY NMR OF 1-209.
RX MEDLINE=97172562; PubMed=9020082;
RA Sattler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E.,
RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
RA Thompson C.B., Fesik S.W.;
RT "Structure of Bcl-XL-Bak peptide complex: recognition between
RT regulators of apoptosis.";
RL Science 275:983-986(1997).
```

[8]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.
RX MEDLINE=96256675; PubMed=8692274;
RA Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
RA Yoon H.S., Nettlesheim D., Chang B.S., Thompson C.B., Wong S.L.,
RA Ng S.L., Fesik S.W.;
RT "X-ray and NMR structure of human Bcl-xL, an inhibitor of programmed
RT cell death.";
RL Nature 381:335-341(1996).
[9]
RP CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.
RX MEDLINE=98118550; PubMed=9435230;
RA Clem R.J., Cheng E.H.-Y., Karp C.B., Karsch D.G., Ueno K.,
RA Takahashi A., Kastan M.B., Griffin D.E., Earnshaw W.C., Velluona M.A.,
RA Hardwick J.M.;
RT "Modulation of cell death by Bcl-xL through caspase interaction.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).
CC -!- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-x(L) anti-
CC apoptotic activity is inhibited by association with SIVA isoform
CC 1. Inhibits activation of caspases (by similarity). Appears to
CC regulate cell death by blocking the voltage-dependent anion
CC channel (VDAC) by binding to it and preventing the release of the
CC caspase activator, cytochrome c, from the mitochondrial membrane.
CC The Bcl-x(S) isoform promotes apoptosis.
CC -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2.
CC Heterodimerization with BAX does not seem to be required for anti-
CC apoptotic activity. Isoform Bcl-x(L) binds to SIVA isoform 1.
CC -!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC envelope (by similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC 1. Event=Alternative splicing; Named isoforms=3;
CC Name=Bcl-X(L);
CC IsoId=Q07817-1; Sequence=Displayed;
CC Name=Bcl-X(S);
CC IsoId=Q07817-2; Sequence=VSP_000515;
CC Name=Bcl-X(beta);
CC IsoId=Q07817-3; Sequence=VSP_000516;
CC -!- TISSUE SPECIFICITY: Bcl-x(S) is expressed at high levels in cells
CC that undergo a high rate of turnover, such as developing
CC lymphocytes. In contrast, Bcl-x(L) is found in tissues containing
CC long-lived postmitotic cells, such as adult brain.
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; 223116; CA80662.1; -;
CC EMBL; 223115; CA80661.1; -;
CC EMBL; U72398; AAB17354.1; -;
CC EMBL; BC019307; AAH19307.1; -;
CC PIR; B47537; B47537;
CC PDB; 1XKL; 29-OCT-97.
CC PDB; 1MAZ; 21-APR-97.
CC PDB; 1G5J; 07-FEB-01.
CC PDB; 1G5M; 21-MAR-01.
CC PDB; 1GHI; 13-JUN-01.

Genew; HGNC:992; BCL2L1.
DR MIM; 600339; -;
DR GO; GO:0005739; C:mitochondrion; TAS.
DR GO; GO:0008189; P:apoptosis inhibitor activity; TAS.
DR GO; GO:0008916; P:anti-apoptosis; TAS.
DR GO; GO:0008637; P:apoptotic mitochondrial changes; TAS.
DR GO; GO:0008634; P:negative regulation of survival gene products; TAS.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAM; TIGR00865; bcl-2; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PSS0063; BH4_2; 1.
KM Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
KW 3D-structure.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226 POTENTIAL.
FT SITE 61 62 CLEAVAGE (BY CASPASE-1).
FT VARSPPLIC 126 188 MISSING (in isoform Bcl-X(S)).
FT FTID-VSP 000515.
FT DTVELYGNNAAESRKQGERFNRWFLTGMTVAGVVLGSL
FT FSRK -> VRTPLVCPFLASGQSPSTALLLYLFLLOWVI
FT VGDVDS (in isoform Bcl-X(beta)).
FT FTID-VSP 000516.
FT D->A: NO CLEAVAGE BY CASPASE-1 NOR BY
FT CASPASE-3.
FT MUTAGEN 61 61 FRD->VRA: NO HETERODIMERIZATION WITH BAX.
FT MUTAGEN 131 133 VMD->AIL: LOSS OF ANTI-APOPTOTIC
FT MUTAGEN 135 137 ACTIVITY.
FT MUTAGEN 138 140 GRI->ELN: LOSS OF ANTI-APOPTOTIC
FT ACTIVITY.
FT MUTAGEN 138 138 G->A: NO HETERODIMERIZATION WITH BAX.
FT MUTAGEN 148 148 G->E: NO HETERODIMERIZATION WITH BAX.
FT MUTAGEN 156 156 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.
FT MUTAGEN 176 176 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.
FT MUTAGEN 188 189 WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY
Query Match 42.1%; Score 424.5; DB 1; Length: 233;
Best Local Similarity 40.9%; Pred. No. 5.7e-31;
Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 4;
QY 11 RALVADFVGYRLRQKGY-----V 28
DB 6 RELVDFLYKLSQKYSWSQFSDEENRTEAPEGTSSEMETPSAINGPSWHLADSAV 65
QY 29 CGAGPGEPPAD-----PLHQAMRAAGDEFETRFRRTFSDLAALHVTGSSAQQRFT 80
DB 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDFEELRYRRAFSDLTSQLHTPGYVQSFE 124
QY 81 QVSDLELFOGPPWGRVLVAFVFGALCAESVNEKEPLVGQVQDWMVAYLETRLDWHS 140
DB 125 QVYNELFRDGVNMGRIVAFVFGALCVESVDKMCQVLSRIAAMWATYLNHDHLEPWIQE 184
QY 141 SGWAEFTALYGDGALEEARLRE--GNWASVRTVLGTGAVALGAL 183
DB 185 NGNDTFVELYGNNAESRKQGERFNRWFLTGMTVAGVVLGSL 229
RESULT 9
BCL2_CHECK STANDARD; PRT; 233 AA.
ID -BCL2_CHECK

AC Q00709;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2 OR BCL-2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92375724; PubMed=1508712;
 RA Eguchi Y., Swert D.L., Tsujimoto Y.;
 RT "Isolation and characterization of the chicken bcl-2 gene: expression
 RT in a variety of tissues including lymphoid and neuronal organs in
 RT adult and embryo.";
 RL Nucleic Acids Res. 20:4187-4192(1992).
 RY [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell lymphoma;
 RX MEDLINE=92379084; PubMed=1511008;
 RA Cazals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;
 RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken
 RT homologue of the Bcl-2 oncoprotein.";
 RL Biochim Biophys. Acta 1132:109-113(1992).
 CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
 CC including factor-dependent lymphomatopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (APAF-1).
 CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAK, BAK and
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
 CC domains, and is necessary for anti-apoptotic activity (By
 CC similarity). Also interacts with APAF-1 and RAFL-1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
 CC membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -!- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen,
 CC kidney, heart, ovary and brain, with the highest levels in the
 CC thymus. In the embryo, highly levels expressed in all tissues with
 CC high levels in the bursa of fabricius.
 CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
 CC for interaction with RAFL-1 (By similarity).
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D11382; BAA01978.1; ..
 DR EMBL; D11381; BAA01978.1; JOINED.
 DR EMBL; Z11361; CAA78018.1; ..
 DR PIR; A37332; A37332.
 DR PIR; S24390; S24390.
 DR HSP; Q07817; IMAZ.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR003093; Bcl2_BH4.
 DR InterPro; IPR002475; Bcl2_family.
 DR InterPro; IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.

DR SMART; SM00265; BH4; 1.
 DR TIGRFS; TIGR00865; bcl-2; 1.
 DR PROSITE; PSS0062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4; 1.
 DR PROSITE; PS0063; BH2_2; 1.
 KW Apoptosis; Transmembrane; Mitochondrion.
 FT DOMAIN 10 30 BH4.
 FT DOMAIN 87 101 BH3.
 FT DOMAIN 130 149 BH1.
 FT DOMAIN 181 196 BH2.
 FT TRANSMEM 208 228 POTENTIAL.
 FT CONFLICT 64 64 E -> S (IN REF. 2).
 FT CONFLICT 67 82 GSAASEVPPAEGLRP -> ARLLLVRCPLRGCA
 FT CONFLICT 121 121 H -> T (IN REF. 2).
 FT CONFLICT 139 139 G -> V (IN REF. 2).
 FT CONFLICT 233 AA; 525255SACB6E4C3D CRC64;
 SQ SEQUENCE 233 AA; 25687 MW; 525255SACB6E4C3D CRC64;
 Query Match 41.7%; Score 420.5; DB 1; Length 233;
 Best Local Similarity 37.6%; Pred. No. 1.3e-30;
 Matches 86; Conservative 33; Mismatches 61; Indels 49; Gaps 4;
 QY 9 DTPALVADFVGVRLRQKGYVCGAG-----PGEPPAADP----- 41
 DB 10 DNREIVLVKVIHYKLSQRGYDMAAGEDRPVPAPAPAPAAVAAGASSHHRPEPPGSA 69
 QY 42 -----LHQAARAGDETFRRFTFSLAAQLHVTGSAQORFTQVSD 84
 DB 70 AASEVPPAEGLRPPAPGVHLARQAGDEFRRYQDFQMSQLHLTPFAGRFVAVVE 129
 QY 85 ELFGQGNMGRVVAFFVFGAALCAESVNMKEMPLVQGVQVDMVAYLETSLADVTHSSGGM 144
 DB 130 ELPRDGVNMGRIVARPEFGVGVNEMSPVLDN:ATWMTVYLNRHLNKHQIDNGCM 189
 QY 145 APTALYGGALAEARLRREGKVASVTVLTGAVALGALVTVGAFASK 193
 DB 190 DAFVELYGN----SMRPLDFSMISLKTLS-LVLVGACITLGLAYLGHK 233
 RESULT 10
 ID_BCL2_BOVIN STANDARD; PRT; 229 AA.
 AC O02718;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Holstein; TISSUE=Thymus;
 RA Reyes R.A., Cockerell G.L.;
 RT "Bovine leukemia virus associated-leukemogenesis is correlated
 RT with suppression of programmed cell death and increased expression
 RT of Bcl-2.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
 CC including factor-dependent lymphomatopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (APAF-1) (By similarity).
 CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAK and
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2

domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with RAF-1 and RAF-2 (By similarity).

-!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum (By similarity).

-!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).

-!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptotic activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphatase 2A (Pp2A) (By similarity).

-!- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

-!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

-!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

-!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

-!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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CC  DR  EYBL; U32434; AAB53319.1; --
CC  DR  HSSP; Q07817; IMAZ.
CC  DR  InterPro; IPR000712; Bcl2_BH.
CC  DR  InterPro; IPR003093; Bcl2_BH4.
CC  DR  InterPro; IPR002475; BCL2_family.
CC  DR  InterPro; IPR004725; Bcl2_reg.
CC  DR  Pfam; PF00452; Bcl-2; 1.
CC  DR  Pfam; PF02180; BH4; 1.
CC  DR  SMART; SM00337; BCL; 1.
CC  DR  SMART; SM00265; BH4; 1.
CC  DR  TiGReMS; TIGR00865; bcl-2; 1.
CC  DR  PROSITE; PS50062; BCL2_FAMILY; 1.
CC  DR  PROSITE; PS01080; BH1; 1.
CC  DR  PROSITE; PS01258; BH2; 1.
CC  DR  PROSITE; PS01259; BH3; 1.
CC  DR  PROSITE; PS01260; BH4; 1; 1.
CC  DR  PROSITE; PS50063; BH4-2; 1.
CC  DR  Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
CC  KW  BH4.
CC  FT  DOMAIN 10 30
CC  FT  DOMAIN 64 68
CC  FT  DOMAIN 69 72
CC  FT  DOMAIN 83 97
CC  FT  DOMAIN 126 145
CC  FT  DOMAIN 177 192
CC  FT  DOMAIN 202 223
CC  FT  SITE 34 35
CC  FT  MOD RES 63 63
CC  FT  SEQUENCE 229 AA; 25099 MW; AD1D00AF98FF1D CRC64.
CC  SQ  CLEAVAGE (BY CASPASES) (BY SIMILARITY).
CC  SQ  PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

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CY      89  GGPNMGRJLVAFVFGAALCAESVNMKEPLVGQVQDMMVAYLETRLADWIHSSGGWAET 149
D5      130  DGVNMGRIVAFVFGGVMCVSVNRENSPLVDLSIALWMTLYLRHLHTMTIQDNGGWDATV 189
QY      149  ALYDGALEAEARRUREGNWASVRTVLTGAVALGALVTVGAFVASK 193
D5      150  ELYG----PSMRPLDFSW-SLKALLSLAL-VGACITLGAYLGHK 229

RESULT 11
ID      BCL2_RAT
CD      BCL2_RAT STANDARD; PRT; 236 AA.
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Apoptosis regulator Bcl-2.
GN      BCL2 OR BCL-2.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxId=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=94193015; PubMed=8144041;
RA      Sato T., Irie S., Krajewski S., Reed J.C.;
RT      "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
RL      Gene 140:291-292(1994) [2]
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Spague-Dawley; TISSUE=Ovary;
RX      MEDLINE=95129487; PubMed=7828536;
RA      Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT      "Expression of members of the bcl-2 gene family in the immature rat
RT      ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT      cell apoptosis is associated with decreased bax and constitutive
RT      bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL      Endocrinology 136:232-241(1995) [3]
RN      [3]
RP      SEQUENCE OF 19-172 FROM N.A.
RX      MEDLINE=95059917; PubMed=7969891;
RA      Casiren E., Onga Y., Berzaghi M.P., Tzimogiorgis G., Thoenen H.,
RA      Lindholm D.;
RT      "bcl-2 messenger RNA is localized in neurons of the developing and
RT      adult rat brain.";
RL      Neuroscience 61:165-177(1994).
CC      -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC      including factor-dependent lymphohematopoietic and neural cells.
CC      Regulates cell death by controlling the mitochondrial membrane
CC      permeability. Appears to function in a feedback loop system with
CC      caspases. Inhibits caspase activity either by preventing the
CC      release of cytochrome c from the mitochondria and/or by binding to
CC      the apoptosis-activating factor (APAF-1).
CC      -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC      Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC      domains, and is necessary for anti-apoptotic activity (By
CC      similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC      -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC      membrane of the nuclear envelope and the endoplasmic reticulum.
CC      -!- TISSUE SPECIFICITY: Expressed in a variety of tissues, with
CC      highest levels in reproductive tissues. In the adult brain,
CC      expression is localized in mitral cells of the olfactory bulb,
CC      granule and pyramidal neurons of hippocampus, pontine nuclei,
CC      cerebellar granule neurons, and in ependymal cells. In prenatal
CC      brain, expression is higher and localized in the neuroepithelium
CC      and in the cortical plate.
CC      -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC      for interaction with RAF-1 (By similarity).
CC      -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC      anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC      on Ser-70 by PKC is required for the anti-apoptosis activity and

```

occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

-- PTM: Phosphorylated by protein phosphatase 2A (PP2A) (By similarity).

-- CLEAVAGE: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

-- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

-- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

-- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

-- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

-- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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EMBL; L14680; AAAS3662.1; -.
EMSL; U34964; AAA77687.1; -.
EMBL; S74122; -; NOT_ANNOTATED_CDS.
PIR; I53744; I53744.
PIR; I67432; I67432.
HSSP; Q07817; 1MAZ.
InterPro; IPR000712; Bcl2_BH.
InterPro; IPR003093; Bcl2_BH4.
InterPro; IPR02475; Bcl2_family.
InterPro; IPR0C4725; Bcl2_reg.
Pfam; PF00452; Bcl-2_1.
Pfam; PF02180; BH4_1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
TIGRFAMs; TIGR00865; bcl-2_1.
PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
PROSITE; PS50063; BH4_2; 1.
Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
DOMAIN 10 30 BH4.
DOMAIN 90 104 BH3.
DOMAIN 133 152 BH1.
DOMAIN 184 199 BH2.
TRANSMEM 209 230 POTENTIAL.
SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
MOD_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
CONFLICT 42 42 A -> R (IN REF. 1).
CONFLICT 157 157 E -> G (IN REF. 1).
CONFLICT 164 164 S -> Y (IN REF. 2).
CONFLICT 212 212 L -> Q (IN REF. 2).
SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;

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142 GGWAFTYAGSGLAEARRLRREGNWSAVRTVITGVAIVGALVTVGAFPAK 193
|||||
190 GGWDADFVELYG---PSMRPLFDPSWLSLTKLTLALL-VGACITLTGAYLGHK 236

RESULT 12
BCL2_MOUSE
ID BCL2_MOUSE STANDARD; PRT; 236 AA.
AC P10417; P10418;
DC 01-VAR-1989 (Rel. 10, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2 OR BCL-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC
RC STRAIN=BALE/C; TISSUE=Liver;
RC MEDLINE=87187643; PubMed=3032455;
RA Negrini M., Sillini E., Korak C., Tsujimoto Y., Croce C.M.;
RT "Molecular analysis of mbcl-2: structure and expression of the murine
RT gene homologous to the human gene involved in follicular lymphoma.";
RN Cell 49:455-463(1987).
RN [2]
RP REVISIONS TO 221-222.
RP MEDLINE=92375224; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RT in a variety of tissues including lymphoid and neuronal organs in
RT adult and embryo.";
RN Nucleic Acids Res. 20:4187-4192(1992).
RN [3]
RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.
RP MEDLINE=97277291; PubMed=9115213;
RA Ito T., Deng X., Carr B., May W.S. Jr.;
RT "Bcl-2 phosphorylation required for anti-apoptosis function.";
RN J. Biol. Chem. 272:11671-11673(1997).
RN [4]
RP DEPHOSPHORYLATION BY PP2A.
RP MEDLINE=99069407; PubMed=9852076;
RA Deng X., Ito T., Carr B., Mumby M., May W.S. Jr.;
RT "Reversible phosphorylation of Bcl2 following interleukin 3 or
RT bryostatin 1 is mediated by direct interaction with protein
RT phosphatase 2A";
RN J. Biol. Chem. 273:34157-34163(1998).
RC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
RC including factor-dependent lymphohematopoietic and neural cells.
RC Regulates cell death by controlling the mitochondrial membrane
RC permeability. Appears to function in a feedback loop system with
RC caspases. Inhibits caspase activity either by preventing the
RC release of cytochrome c from the mitochondria and/or by binding to
RC the apoptosis-activating factor (APAF-1).
RC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
RC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
RC domains, and is necessary for anti-apoptotic activity (By
RC similarity). Also interacts with APAF-1 and RAF-1.
RC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
RC membrane of the nuclear envelope and the endoplasmic reticulum.
RC -!- ALTERNATIVE PRODUCTS:
RC Name=Alternative splicing; Named isoforms=2;
RC Name=Alpha;
RC IsoId=P10417-1; Sequence=Displayed;
RC Name=Beta;
RC IsoId=P10417-2; Sequence=VSP_000513;
RC -!- TISSUE SPECIFICITY: Expressed in a variety of tissues.
RC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
RC for interaction with RAF-1.
RC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
RC on Ser-70 by PKC is required for the anti-apoptosis activity and
RC on Ser-70 by PKC is required for the anti-apoptosis activity and

```


RT CC Generation and initial analyses of more than 15,000 full-length
RT CC human and mouse cDNA sequences.";
RL CC Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [6]
RP SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS
RP NON-HODGKIN'S LYMPHOMA SER-59 AND ILE-93.
RX MEDLINE=92096610; PubMed=1339299;
RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.;
RT "Frequent incidence of somatic mutations in translocated BCL2
RT oncogenes of non-Hodgkin's lymphomas.";
RL Blood 79:229-237 (1992).
RN [7]
RN SUBCELLULAR LOCATION.
RP MEDLINE=942339528; PubMed=8183370;
RX MEDLINE=91066924; PubMed=2250705;
RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;
RT "Bcl-2 is an inner mitochondrial membrane protein that blocks
RT programmed cell death";
RL Nature 348:334-336 (1990).
RN [8]
RN MUTAGENESIS.
RP MEDLINE=942339528; PubMed=8183370;
RX MEDLINE=91066924; PubMed=2250705;
RA Yin X.-M., Olivai Z.N., Korsmeyer S.J.;
RT "BH1 and BH2 domains of Bcl-2 are required for inhibition of
RT apoptosis and heterodimerization with Bax";
RL Nature 369:321-323 (1994).
RN [9]
RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.
RX MEDLINE=98057466; PubMed=9395403;
RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,
RA Ueno K., Hardwick J.M.;
RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";
RL Science 278:1966-1968 (1997).
RN [10]
RP REVIEW ON PHOSPHORYLATION.
RX MEDLINE=21260650; PubMed=11360354;
RA Ruvolo P.P., Deng X., May W.S.;
RT "Phosphorylation of Bcl2 and regulation of apoptosis.";
RL Leukemia 15:515-522 (2001).
RN [11]
RP PHOSPHORYLATION BY ASK1/JNK1.
RX MEDLINE=20036804; PubMed=10567572;
RA Yamamoto K., Ichijo H., Korsmeyer S.J.;
RT "BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal
RT protein kinase pathway normally activated a G2/M.";
RL Mol. Cell. Biol. 19:8469-8478 (1999).
CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1).
CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (by
CC similarity). Also interacts with APAF-1 and RAF-1.
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC {isoId=PI0415-1; Sequence=Displayed;
CC Name=Beta;
CC {isoId=PI0415-2; Sequence=VSP 000512;
CC -!- TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAF-1.
CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle. In the absence of
CC growth factors, Bcl2 appears to be phosphorylated by other protein
CC kinases such as ERKs and stress-activated kinases.

CC Dephosphorylated by protein phosphatase 2A (PP2A) (by similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -!- DISEASE: Involved in follicular lymphoma (FL) (also known as type
CC II chronic lymphatic leukemia) by a chromosomal translocation
CC t(14;18)(q32;q21) which involves BCL2 and immunoglobulin gene
CC regions. Bcl2 mutations found in non-Hodgkin's lymphomas carrying
CC the chromosomal translocation could be attributed to the Ig
CC somatic hypermutation mechanism resulting in nucleotide
CC transitions.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -!- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.; BCL2ID49.html".
CC WWW="http://www.infobio.fr/services/Chromancer/Genes/BCL2ID49.html".
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M13994; AAA51813.1; ALT_SEQ.
DR EMBL: M13995; AAA51814.1; ALT_SEQ.
DR EMBL: M14745; AAA35591.1;
DR EMBL: X06487; CAA29778.1;
DR EMBL: EC027258; AAH27258.1;
DR EMBL: S72602; AAD14111.1; ALT_SEQ.
DR PIR: C37332; TVHUA1.
DR PDB: 1G5M; 21-MAR-01.
DR PDB: 1GUH; 13-JUN-01.
DR Genew: HGNC:990; BCL2.
DR MIM: 151430; -.
DR GO: GO:0005743; C:mitochondrial inner membrane; TAS.
DR GO: GO:0008189; P:apoptosis inhibitor activity; TAS.
DR GO: GO:0006916; P:anti-apoptosis; TAS.
DR GO: GO:0006959; P:humoral immune response; TAS.
DR GO: GO:0008285; P:negative regulation of cell proliferation; TAS.
DR GO: GO:0007048; P:oncogenesis; TAS.
DR GO: GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; BCL2 family.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF0180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PS00062; BCL2 FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS00063; BH4_2; 1.
KW Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane;
KW Mitochondrion; Phosphorylation; Chromosomal translocation;
KW Polymorphism; Disease mutation; 3D-structure.

Query Match 40.5%; Score 408.5; DB 1; Length 239;
Best Local Similarity 36.6%; Pred. No. 1.6e-29;
Matches 86; Conservative 35; Mismatches 59; Indels 55; Gaps 5;
QY 9 DTRALVADVGVRQRQKGVCGAG-----PGE----- 35
DB 10 DNRREIMVYIIHKLSQRGYWDAGVGNAAPGAPAGIFSSQDGHTPHAASDPVART 69

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CC 36 -----GPAADP-----LHQAVRAAGDBFETFRRTFTSDLAALQHLVTPGSACOR 78
CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC 70 SPLQTPAAPGAAGPALSPVFPVHLLRLQAGDDFSRRYRDFPMSSSQLHLTPFTARGR 129
CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC 79 FTQVSDLELFOGPNNGRLVAFVFGAALCAESVNKMEPLVGQVQDMMVAYLETRLADWI 138
CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC 130 FATVVEELFRDGVNMGRIVAFFEFGGVNCVSVNREMSPLVDNIALMWTYLRHLHTW 189
CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC 139 HSSGWAFFTLVGDGALLEEARREGNWSVRTLTCALVALGALVTVGAFPAASK 193
CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC 190 QNGGDAFVELYG-----PSMRPLDFPSWLSKLLSLAL-VGACITLGTLYLGHK 239
CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
ID BCL2 CRILO STANDARD; PRT; 236 AA.
AC Q95J38;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=20431763; PubMed=10973819;
RA Tomicic M.T., Christmann M., Kaina B.;
RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
RT protein."
RL Biochem. Biophys. Res. Commun. 275:899-903(2000).
RN [2]
RP SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES.
RX MEDLINE=21092839; PubMed=11281062;
RA Tomicic M.T., Kaina B.;
RT "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
RT and caspase-3."
RL Biochem. Biophys. Res. Commun. 281:404-408(2001).
CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphomatopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1) (By similarity).
CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RAFA-1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAFA-1 (By similarity).
CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle (By similarity). In
CC the absence of growth factors, Bcl2 appears to be phosphorylated
CC by other protein kinases such as ERKs and stress-activated kinases
CC (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A);
CC (By similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

```

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CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AJ2711720; CAB92245.1; -.
CC PIR: JC7383; JC7383.
CC RSP: Q07817; 1MAZ.
CC InterPro: IPR00712; Bcl2 BH.
CC InterPro: IPR003093; Bcl2 BH4.
CC InterPro: IPR002475; BCL2_family.
CC InterPro: IPR004725; BCL2_reg.
CC Pfam: PFC0452; Bcl-2; 1.
CC Pfam: PFC2180; BH4; -.
CC SMART: SM00337; BCL; 1.
CC SMART: SM00265; BH4; 1.
CC TIGRfam: TIGR00865; bcl-2; 1.
CC PROSITE: PS50062; BCL2_FAMILY; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; -.
CC PROSITE: PS01259; BH3; 1.
CC PROSITE: PS01260; BH4; 1.
CC PROSITE: PS50063; BH4_2; 1.
CC Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
KW DOMAIN 10 30
FT DOMAIN 90 104 BH4.
FT DOMAIN 133 152 BH1.
FT DOMAIN 184 199 BH2.
FT TRANSMEM 209 230 POTENTIAL.
FT SITE 64 65 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).
FT MOD_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ SEQUENCE 236 AA; 26491 MW; BECADFIEF337228 CRC64;

Query Match 39.5%; Score 399; DB 1; Length 236;
Best Local Similarity 34.9%; Pred. No. 1.1e-28;
Matches 81; Conservative 35; Mismatches 64; Indels 52; Gaps 3;

QY 9 DTRALVADFVGLRQKY-----
DB 10 DNRREIMKYIHYKLSQRYGWDVGDVDAAPLGAAPTGFQFQPSNPTPAVHRDMAART 69
QY 28 -----VCGAGFGECPAADPLHQAARAGDEFETFRFTSDLAALQHLVTPGSACORFTQ 81
DB 70 SPLRPIVATTGTLSPVPVHLLRLRAGDDFSRRYRDFPMSSSQLHLTPFTARGRAT 129
QY 82 VSEDLFOGPNNGRLVAFVFGAALCAESVNKMEPLVGQVQDMMVAYLETRLADWIHSS 141
DB 130 VVEELFRDGVNMGRIVAFFEFGGVNCVSVNREMSPLVDNIALMWTYLRHLHTW:QDN 189
QY 142 GMAEFETLYGDGALLEEARREGNWSVRTLTCALVALGALVTVGAFPAASK 193
DB 190 QNGGDAFVELYG-----PSMRPLDFPSWLSKLLSLAL-VGACITLGTLYLGHK 236

RESULT 15
AR:: XENLA
ID AR11 XENLA STANDARD; PRT; 204 AA.
AC Q91828;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptosis regulator R11 (XR11).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]

```

RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=95331613; PubMed=7607538;
RA Cruz-Reyes J., Iata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
cell-survival genes.";
RL Gene 158:171-179(1995).
CC -!- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
CC -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -!- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND
CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X82461; CAAS7844.1; -.
DR HSP: Q07817; IMRZ.
DR InterPro: IPR00712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF0452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRPFAMS: TIGR00865; bcl-2; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR Apoptosis; Transmembrane.
KW DOMAIN 101 120 BH1.
FT DOMAIN 152 167 BH2.
FT TRANSMEM 151 196 POTENTIAL.
SQ SEQUENCE 204 AA; 23379 MW; 38FC6BE6DDA4CA03 CEC64;

Query Match 36.3%; Score 366; DB 1; Length 204;
Best Local Similarity 41.5%; Pred. NO. 8.5e-26;
Matches 81; Conservative 25; Mismatches 63; Indels 26; Gaps 4;

QY 10 TPALVADVGYRLRQKGYVC-----GAGPGGPAADPLHCAMR 47
DB 5 SRDLVEKVFVKLSQ-NEACKRFSNPNPMLPEPSTSRPGSGATCGIVEEVQLALL 63
QY 48 AAGDEFETRFRTRTSDLAQLHVTFGSAQCRFTQVSDLFQGGPNWGLVAFVFGAALC 107
DB 64 EATEEFELRYQAFSDLTSQLHITQDTAQGFQCVMGELFRDGTNWGRVAFPSFGAALC 123
QY 108 AESVNVKMEPLVGVQVDKRVAYLETRLDWTHSSGNAEFTALYDGALEARLRE--G 165
DB 124 VESAKNETDLPRIQVQWVNYLEHTLQFVQENGWGEAFVGLYGNKNAQAQSRSEQRFG 183
QY 166 NWASVRTVLITGAVAL 180
DB 184 RLITI-VMLTGVFAL 197

Search completed: October 24, 2003, 10:46:48
Job time : 14.5 secs

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OM protein - protein search, using sw model

Run on: October 24, 2003, 10:43:10 ; Search time 62 Seconds

(without alignments)
803.293 Million cell updates/sec

Title: US-09-925-674A-9

Perfect score: 1009

Sequence: 1 MATPASTPTPALVADFGV.....LTGAVALGALVTVGAFASK 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 3

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first: 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_minc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_todent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1002	99.3	193	11	O88996
2	965	95.6	193	11	Q8CGU4
3	767	76.0	178	11	O9CYW5
4	767	76.0	178	11	O8CFR2
5	436.5	43.3	233	6	Q9MYW4
6	432.5	42.9	233	11	O35844
7	429.5	42.6	233	6	O8SQ42
8	428.5	42.5	233	6	Q9N1A2
9	425.5	42.2	233	6	Q9MZS7
10	409	40.5	236	11	O8BQK4
11	401	39.7	180	6	Q9BDD5
12	401	39.7	217	11	O39N35
13	399.5	39.6	180	6	Q9BDX7
14	397	39.3	238	13	Q90Z98
15	395	39.1	236	11	Q923R6
16	394.5	39.1	235	6	Q81008

17	371.5	36.8	188	11	O9QWX2
18	371.5	36.8	235	11	O35843
19	369.5	36.6	188	4	Q9H1R6
20	368	36.5	204	13	Q90ZK2
21	350	34.7	185	6	Q8M0B1
22	347	34.4	219	11	O99N36
23	339.5	33.6	199	11	O8CSP0
24	296	29.3	89	13	O8UWJ1
25	187	18.5	209	11	O9JK59
26	182	18.0	170	11	O9WU15
27	182	18.0	209	11	O8C264
28	177.5	17.6	192	13	Q919N4
29	175.5	17.4	221	13	O98U13
30	173.5	17.2	190	4	Q8NFF3
31	165.5	16.4	125	4	O9H1R5
32	163	16.2	235	5	O967D2
33	162	16.1	158	11	O9R1B3
34	157.5	15.6	163	6	Q9MZS6
35	156.5	15.5	173	11	O8K3J2
36	154	15.3	173	4	Q8WZ49
37	154	15.3	173	11	O9JKL3
38	151	15.0	67	6	Q8MJB3
39	149	14.8	192	6	O8SQ43
40	148.5	14.7	218	5	Q9N754
41	148	14.7	192	6	O8HYU5
42	147.5	14.6	179	4	O9NYG7
43	145	14.4	149	6	O9GMG7
44	144	14.3	177	13	Q90ZN1
45	142	14.1	211	13	Q9W6F1

ALIGNMENTS

RESULT 1

O88996 PRELIMINARY; PRT: 193 AA.
AC O88996; 01-NOV-1998 (TREMELrel. 08, Created)
CT 01-NOV-1998 (TREMELrel. 08, Last sequence update;
DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
DE BCL-W.
GN BCL-W.
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN:Sprague-Dawley; TISSUE=Brain;
RC MEDLINE=99292146; PubMed=10366024;
RA Hamner S., Skoglosa Y., Lindholm D.;
RT "Differential expression of bcl-w and bcl-x messenger RNA in the
RT developing and adult rat nervous system.";
RL Neuroscience 91:673-684(1999).
DR EMBL: AF096291; AAC64200.1; .
DR HSSP: Q07817; 1MAZ.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR 2fam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR PROSITE: PS00062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS00063; BH4_2; 1.
SQ SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;

Query Match 99.3%; Score 1002; DB 11; Length 193;
Best Local Similarity 99.0%; Pred. No. 1.2e-81;


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Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MATPASTPTDTRALVADFGYRLRQKGYVCGAGGPGGAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASTPTDTRALVADFGYRLRQKGYVCGAGGPGGAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHVTGSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESVKNKMEPLVG 120
DB 61 FSDLAQLHVTGSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESVKNKMEPLVG 120
QY 121 QVQDMWVAYLETRLADWTHSSGWAEEFTALYCGGALEBARLRREGNWSVRLTGTGAVAL 180
DB 121 QVQDMWVAYLETRLADWTHSSGWAEEFTALYCGGALEBARLRREGNWSVRLTGTGAVAL 180
QY 181 GALVTGGAFFASK 193
DB 181 GALVTGGAFFASK 193

RESULT 2
ID Q8CGL4 PRELIMINARY; PRT; 193 AA.
AC Q8CGL4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Bcl2-like protein 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RT "Extraction from neonatal mouse skin after IGF-1 stimulation.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RD EMBL; AY170344; AAC13177.1;
SQ SEQUENCE 193 AA; 20950 MW; 258AC1818166DFA0 CRC64;

Query Match 95.6%; Score 965; DB 11; Length 193;
Best Local Similarity 96.4%; Pred. No. 2,3e-78;
Matches 186; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 MATPASTPTDTRALVADFGYRLRQKGYVCGAGGPGGAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASTPTDTRALVADFGYRLRQKGYVCGAGGPGGAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHVTGSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESVKNKMEPLVG 120
DB 61 FSDLAQLHVTGSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESVKNKMEPLVG 120
QY 121 QVQDMWVAYLETRLADWTHSSGWAEEFTALYCGGALEBARLRREGNWSVRLTGTGAVAL 180
DB 121 QVQDMWVAYLETRLADWTHSSGWAEEFTALYCGGALEBARLRREGNWSVRLTGTGAVAL 180
QY 181 GALVTGGAFFASK 193
DB 181 GALVTGGAFFASK 193

RESULT 3
ID Q9CYW5 PRELIMINARY; PRT; 178 AA.
AC Q9CYW5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Bcl2-like 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RD EMBL; AK013244; BAB28740.1;
SQ SEQUENCE 178 AA; 19147 MW; E2D4C3F79528E9D7 CRC64;

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NCBI_TaxID=10090;
QY 1 MATPASTPTDTRALVADFGYRLRQKGYVCGAGGPGGAADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASTPTDTRALVADFGYRLRQKGYVCGAGGPGGAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHVTGSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESVKNKMEPLVG 120
DB 61 FSDLAQLHVTGSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESVKNKMEPLVG 120
QY 121 QVQDMWVAYLETRLADWTHSSGWAEEFTALYCGGALEBARLRREGNWSVRLTGTGAVAL 150
DB 121 QVQDMWVAYLETRLADWTHSSGWAEEFTALYCGGALEBARLRREGNWSVRLTGTGAVAL 150

RESULT 4
ID Q8CFR2 PRELIMINARY; PRT; 178 AA.
AC Q8CFR2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Bcl2-like 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;

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RA Strausberg R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC040369; AAH0369.1; -; E2C3F3F79528E9D7 CRC64;
 SQ SEQUENCE 178 AA; 19119 MW; 25986 MW; 12F0F3C344D53F93 CRC64;

Query Match 76.0%; Score 767; DB 11; Length 178;
 Best Local Similarity 96.0%; Pred. No. 9.9e-61;
 Matches 144; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MATPASTTDTALVADVGVYLRKGVYCGAGGEGPAADPLHOAVRAAGDEFETFRRT 60
 DB 1 MATPASTTDTALVADVGVYLRKGVYCGAGGEGPAADPLHOAVRAAGDEFETFRRT 60
 QY 61 PSDLAALQHVTPGSAQQRFTQVSDDELFGGPNWGRVAVFFVFGAALCAESVNKEMEPLVG 120
 DB 61 PSDLAALQHVTPGSAQQRFTQVSDDELFGGPNWGRVAVFFVFGAALCAESVNKEMEPLVG 120
 QY 121 QVQDMWVAYLETRLADMTIHSSGGWNAEPTAL 150
 DB 121 QVQDMWVAYLETRLADMTIHSSGGWVRSSQL 150

RESULT 5
 QMYW4 PRELIMINARY; PRT; 233 AA.

AC Q9MYW4;
 DT 01-OCT-2000 (TRENBLrel. 15, Created;
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Bcl-X.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxId=9986;
 RN [1];
 RP SEQUENCE FROM N.A.
 RA Knott J.C., Robertson L., James E.R.;
 RT "Rabbit Bcl-X";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY005133; AAF89137.1; -;
 DR HSSP; P53563; IAF3.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR003093; Bcl2_BH4.
 DR InterPro; IPR002475; Bcl2_family.
 DR InterPro; IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4; 1.
 DR PROSITE; PS00063; BH4_2; 1.
 SQ SEQUENCE 233 AA; 25986 MW; 12F0F3C344D53F93 CRC64;

Query Match 43.3%; Score 436.5; DB 6; Length 233;
 Best Local Similarity 41.5%; Pred. No. 4.5e-31;
 Matches 93; Conservative 23; Mismatches 57; Indels 5; Gaps 4;
 QY 11 RALVADFGVYLRKGVYV-----GAG-----PGEPPAA 39
 DB 6 RELVDFLSYKLSQKGYWSQFSDVEENRTAEPTGEMETPSAINGNPANHPADSPAV 65
 QY 40 D-----PLHQAVRAAGDEFETFRRTFSDLAALQHVTPGSAQQRFTQ 81
 DB 66 NGATGSSSLDAREVIPMTAVKQALREAGDEFELRYRAFSDLTSQHLITPGTAYQSFEQ 125
 QY 82 VSDLEFGGPNWGRVAVFFVFGAALCAESVNKEMEPLVGQVQDMWVAYLETRLADMTIHSS 141
 DB 126 VVNELFRDGVNWRIVAVFFSGGALCVESVDKEMQVLVSRIASMMATYLNHLEPWIOEN 185

QY 142 GGMAEFTALYGDGALAEABRLRE--GNWASVRTVLTGVALGAL 183
 DB 186 GGDWTFVELYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229
 RESULT 6
 Q35844 PRELIMINARY; PRT; 233 AA.
 AC Q35844;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Bcl-XL.
 GN BCL2L.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1];
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6/CBA; TISSUE=Thymus;
 RC MEDLINE=98051053; PubMed=9190687;
 RA Yang X.-F., Weber G.F., Cantor H.;
 RT "A novel Bcl-x isoform connected to the T cell receptor regulates
 apoptosis in T cells";
 RL Immunity 7:629-639(1997).
 DR EMBL; U51278; AAC53459.1; -;
 DR HSSP; P53563; IAF3.
 DR MGD; MGI:88139; Bcl2l.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR003093; Bcl2_BH4.
 DR InterPro; IPR002475; Bcl2_family.
 DR InterPro; IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PS00062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4; 1.
 DR PROSITE; PS00063; BH4_2; 1.
 SQ SEQUENCE 233 AA; 26033 MW; 3083F2D8327E072E CRC64;

Query Match 42.9%; Score 432.5; DB 11; Length 233;
 Best Local Similarity 41.3%; Pred. No. 1e-30;
 Matches 93; Conservative 23; Mismatches 56; Indels 53; Gaps 4;
 QY 11 RALVADFGVYLRKGVY-----V 28
 DB 6 RELVDFLSYKLSQKGYWSQFSDVEENRTAEPTGEMETPSAINGNPANHPADSPAV 65
 QY 29 CGAGGEGPAAD-----PLHQAVRAAGDEFETFRRTFSDLAALQHVTPGSAQQRFT 80
 DB 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRAFSDLTSQHLITPGTAYQSFE 124
 QY 81 QVSDLEFGGPNWGRVAVFFVFGAALCAESVNKEMEPLVGQVQDMWVAYLETRLADMTIHSS 140
 DB 125 QVWNELEFRDGVNWRIVAVFFSGGALCVESVDKEMQVLVSRIASMMATYLNHLEPWIOE 184
 QY 141 SGMNAEFTALYGDGALAEABRLREG--NWSASVRTVLTGVALGAL 183
 DB 185 NGGDWTFVDLYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 7
 Q8SQ42 PRELIMINARY; PRT; 233 AA.
 ID Q8SQ42
 AC Q8SQ42;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)


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DR PROSITE; PS50063; BH4.2; 1.
SQ SEQUENCE 233 AA; 25134 MW; 012BFA1382762915 CRC64;

Query Match 42.2%; Score 425.5; DB 6; Length 233;
Best Local Similarity 40.2%; Pred. No. 4.3e-30;
Matches 90; Conservative 24; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADFVGYRLQKGY-----VCGAGP-----GSGPAA 39
DB 6 RELVDFLSYKLSQKGYSGFSQFSDVEENRTPEAGTSDMETPSAINGNSPHLADSPAV 65

QY 40 D-----PLHQMRAGDEFERFRRTFSDLAQLHVTGSAQQRFTQ 81
DB 66 NGATGHSRLDAREVIPMAAKQALREAGDEFEYRRAFSDLTSQHLITPGTAYQSFEQ 125

QY 82 VSEDFQGGPNWGRVLAVFFFGAALCAESVNKMEPLVGQVQDMMVAYLETRLDWIHSS 141
DB 126 VVNELFRQGVNNGRIVAFVFFSGGALCVESVDKEXQVLVSRIATWMTYLNHLEPWIQEN 195

QY 142 GQWAEFTALYDGLAEAEARLFE--GNWASVRYTLTGAVLALGAL 183
DB 186 GQWDTFVELYGNNAAESRKQGFNRWFLTGMTVAGVVLGSL 229

RESULT 10
Q8BQK4
ID Q8BQK4 PRELIMINARY; PRT; 236 AA.
AC Q8BQK4;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE B-cell leukemia/lymphoma 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK049473; BAC33767.1; -.
SQ SEQUENCE 236 AA; 26437 MW; B726SFFAJAA:C718 CRC64;

Query Match 40.5%; Score 409; DB 11; Length 236;
Best Local Similarity 37.1%; Pred. No. 1.3e-28;
Matches 86; Conservative 35; Mismatches 59; Indels 52; Gaps 5;

QY 9 DTRALVADFVGYRLQKGYVCGAG-----PG----- 34
DB 10 ENREIVMKYIHYKLSQSGYEWDAAGDADAAAPLGAAPTPGIFSPQESNPMPAVHRDMAART 69

QY 35 -----EGPAADP-----LHQMRAGDEFERFRRTFSDLAQLHVTGSAQQRFTQ 81
DB 70 SPLRELVNTGTPALSPVPVPHLITLRAGDGFSSRRYRDFRMSQLHLFPFTARGFAI 129

QY 82 VSEDFQGGPNWGRVLAVFFFGAALCAESVNKMEPLVGQVQDMMVAYLETRLDWIHSS 141
DB 130 VVEELFRQGVNNGRIVAFVFFSGGALCVESVNREKSPLVNIALWMTYLNHLEPWIQDN 189

QY 142 GQWAEFTALYDGLAEAEARLFE--GNWASVRYTLTGAVLALGALVTVGAPFASK 193
DB 190 GQWDAFVELY----PSMRPLPFDKSLKLTLLSLAL-VGACITLGYLGHK 236

RESULT 11
Q9BDD5
ID Q9BDD5 PRELIMINARY; PRT; 180 AA.
AC Q9BDD5;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE B-cell leukemia/lymphoma x (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RC Yang X.-F., Cantor H.;
RT "Novel cDNA structure and genomic organization of apoptosis regulatory
RT gene Bcl-x-gamma.>";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF133282; AAK15455.1; -.
DR EMBL; AF133281; AAK15455.1; JOINED.
DR HSSP; P53563; 1AF3.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
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DR SMART; SM00337; BCL; 1.
DR TIGR00865; BCL-2; 1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS02259; BH3; 1.
DR NON_TER; 1.
SQ SEQUENCE 217 AA; 24234 MW; 3B54E809A7DEF18 CRC64;

Query Match 39.7%; Score 401; DB 11; Length 217;
Best Local Similarity 53.5%; Pred. No. 6e-28;
Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;

QY 44 CAMRAAGDEFEFTRRRTFSDLAAQLHVTGSAQGRFTQNSDELFOGQPNWGLVAFVFG 103
DB 72 QALREAGDEFEFLRYRRAFSLTSLQHTPTGATYQSFQVYNELFRDGVNWRIVAFSFG 132
QY 104 AALCAESVNKMEPLVGQVQDMMVAVYETRLADWIIHSSGGWAEFTALYDGGALEEARLR 163
DB 132 GALLCVESVDKEXQVLVRISWMATYNDHLEPWIGENGWDTFVDLYGNNAAESRKQ 191
QY 164 E-GNWSVTRVLTGVALGAL 183
DB 192 ERFNRFLTGTMTAGVVLGSL 213

RESULT 13
ID Q9BDX7 PRELIMINARY; PRT; 180 AA.
AC Q9BDX7;
DR 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Anti-apoptotic regulator Bcl-XL (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1];
RP SEQUENCE FROM N.A.
RA Amillis M., Bouzat J.;
RT "Characterization of the bovine bcl-xL gene and related pseudogenes.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF245487; AAK31306.1; -.
DR HSSP; Q07817; IMAZ.
DR InterPro; IPR00712; Bcl2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; BCL-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
FT NON_TER; 1.
FT NON_TER; 180.
SQ SEQUENCE 180 AA; 20056 MW; 62C4C0B0D055A9EF CRC64;

Query Match 39.6%; Score 399.5; DB 6; Length 180;
Best Local Similarity 47.1%; Pred. No. 6.5e-28;
Matches 82; Conservative 23; Mismatches 58; Indels 11; Gaps 3;

QY 20 YLRQKGVCCAGCEGAAD-----PLHOAMRAAGDEFEFTRRRTFSDLAAQLHVT 71
DB 7 WHELDSPAVNGA-PGHSRSSDAREVPMAAVKQALREAGDEFEFLRYRRAFSLTSLQHT 65
QY 72 PGSAQRFTQNSDELFOGQPNWGLVAFVFGAALCAESVNKMEPLVGQVQDMMVAYLE 131
DB 66 PGTATQSFQVYNELFRDGVNWRIVAFSFGGALCVESVDKEXQVLVSRIA;WMA;TYLN 125
QY 132 TRLADWIIHSSGGWAEFTALYDGGALEEARLR--GNWASVTRVLTGVALGAL 183
DB 126 DHLEPWIGENGWDTFVLYGNNAAESRKQERFNRWF.TGMTVAGVWLLGSJ. 179

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RESULT 14
Q9CZ98 PRELIMINARY; PRT; 238 AA.
AC Q9CZ98;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE BC-XL-like protein 1.
GN BCL2L OR BCL1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=2129061; PubMed=11406282;
RA Chen M.-C., Gong H.-Y., Cheng C., Wang J.-P., Hong J., Wu J.-L.;
RT "Cloning and characterization of zfBCLP1, a Bcl-XL homologue from the
RT zebrafish, Danio rerio(1)";
RL Biochim. Biophys. Acta 1519:127-133(2001).
DR EMBL; AF117837; AAK81706.1; -.
DR ZFIN; ZDB-GENE-010730-1; bcl2l.
DR InterPro; IPR00712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; BCL-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS00063; BH4_2; 1.
DR PROSITE; PS00063; BH4_2; 1.
SQ SEQUENCE 238 AA; 26253 MW; 6E58394933EEFDB CRC64;

Query Match 39.3%; Score 397; DB 13; Length 238;
Best Local Similarity 35.7%; Pred. No. 1.5e-27;
Matches 85; Conservative 29; Mismatches 62; Indels 62; Gaps 6;

QY 11 RALVADFVGYRLRQKYVC-----GAG----- 32
DB 6 RELVVFVFKLSORYPCHNIGLTDNEDGAEENGEGAGATTLVNGTMMNRNASST 65
QY 33 --PGEQPAADPLHQ-----AMRAAGDEFEFTRRRTFSDLAAQLHVTGSAQQR 78
DB 66 GTTPQSPASSPQRTGSSGGLDAVKALRDSANEFELYSRAFNDLSSQLHITPATAYOS 125
QY 79 FTQVSDLEFOGQPNWGLVAFVFGAALCAESVNKMEPLVGQVQDMMVAYLETRLADWI 138
DB 126 PESVNDVFRDGVNWRIVGLFAGGALCVCEKEMSPVGRIAEWMTVYLDNHICPMI 185
QY 139 HSSGGWAEFTALYDGGALEEARLRREG--NWA-SVTRVLTGVALGALVTVGAFFASK 193
DB 186 QSQGQWERFAEIFGKAABESRKQSQSFKKWLPAGMTLLTG-----VVVGGLIAQK 236

RESULT 15
Q923R6 PRELIMINARY; PRT; 236 AA.
AC Q923R6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE B-cell lymphoma protein 2.
GN BCL2.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10030;
RN [1];
RP SEQUENCE FROM N.A.
RA Lai D.Z., Chen W., Wang H.T.;

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RI "Construction of a robust CHO cell line for biopharmaceutical use."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.

DR EMBL: AF494339; AAK92201.1; -
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfam: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS50063; BH4_2; 1.
SQ SEQUENCE 236 AA; 26500 MW; BEDF052EF32CA8B8 CRC64;

Query Match 39.1%; Score 395; DB 1; Length 236;
Best Local Similarity 34.9%; Pred. No. 2.3e-27;
Matches 81; Conservative 33; Mismatches 66; Indels 52; Gaps 3;
QY 9 DTSAJLVDFVGYRLOKGY----- 27
DB 10 DKREIVMKYIHYKLSQRYGVWDVDAAPLGAAPTGGIFSFQPSNPTPAVHRDMAART 69
QY 28 -----VCGAGFGEGPAADPLQAMRAAGDEFETRPRRTFSDLAQLHVTGSAQQRFTQ 81
DB 70 SPLRPVATGPTLSPVPVWHJTLRRAGDDFSRRYRDFAEKSSQLHTPFTARGRFAT 129
QY 82 VSDLPFGGPNKGRUVAFVFGAALCAESVNKEKPELVGQVQDWMVAYLETRLDNIHSS 142
DB 130 VVEELFRDGVNMGRIVAFFEFEGGVNCSVAREKSPVDENIALMTEYLNRHLHTIQDN 189
QY 142 GGAWEFTALYGDGALEEARLRREGNMAVRVLTGAVAGALVTVGAPFASK 193
DB 190 GWDAPVELYG---PSVRPLDFSWLSXTLLNAL-VGACITCTYLGHK 236

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Job time : 63 secs